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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                950
719.5
572
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                         AAB08843
AAY94001
AAE09241
AAE090506
AAB60698
AAY71979
ABB81487
AAE15484
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348.847 Million cell updates/sec
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                                             Human
Human
                                                                                                                        Human BCMA recepto
                                                                                                                                                          Human BAFF recepto
Human B cell matur
                                                                                                                                                                                                                                                                  Amino acid sequenc
A human BCMA prote
Human BCMA protein
        Amino
                                                                                                                                                                                                                                     Human BCMA protein
Human B cell matur
BAFF recepto
acid sequenc
                                                                               B-cell matur
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lymph	AAW75783	19	293	8.1	78.5
uman TACI	AAE09244	22	265	•	78.5
eptor kin	AAR29814	<u>.</u>	857		79
relate	AAW48373	19	1009		79.5
	AAW57891	19	1009	•	79.5
n tyr	AAR98351	17	1009	•	79.5
	AAU09900	23	293		79.5
acid se	AAY23925	20	576		18
Mouse related adhe	AAW48374	19	1009	•	82
e protein	AAW64568	19	1009		82
o	AAW61196	19	1009		82
	AA014136	23	404		83.5
	AAE15492	23	24		90.5
Human JST576 (BAFF	AAE22243	23	266		93
Ztnfr12	ABB81483	23	184		93
Human mature JST57	AAE22242	23	185		94.5
-	AAE22270	23	185		97.5
BAFF	AAE22268	23	185	10.3	99.5
BAFF	AAE22271	23	185		100.5
	AAE22269	23	185		103.5
B-cel	AAE15487	23	21		104
BAFF	AAE22267	23	185		105.5
BAFF r	AAE22266	23	185		106.5
e BAFF recep	AAE22244	23	175		116.5
Mouse Ztnfrl2 prot	ABB81489	23	175		116.5
BCMA - hu	AAE15489	23	281		187
B-cell	AAE15486	23	34		201
	AAE15485	23	51		284
ii), BCM	AAE15488	23	283		286
	AAB60699	22	302		286.5
BCMA - Imm	AAE00507	22	302		286.5
-murine		23	117		311.5
B cell	ᅜ	23	58		323
B cell mat	E154	23	185		572
Murine B cell matu	AAY71980	22	185		572

ALIGNMENTS

DR X	P XX	PA	X PR	XX	ad	X PD	×	PN	X	ŋ ! -3 !	F)	7] ;	×	လွ	XX	X	X	X	XX	DE	XX	ΡŢ	×	AC.	××	ID	RESULT 1
WPI: 2000-558405/51.	Seed B, Ting A;	(GEHO) GEN HOSPITAL CORP.	24-FEB-1999; 99US-0121485.		24-FEB-2000; 2000WO-US04925.	31-AUG-2000.		WO200050633-A1.	יווירב - במרמרדוב בימוושווייות מטוומיוו		Domain 5777		The state of the s	Homo sapiens.		rheumatoid arthritis; inflammatory bowel disease; septic shock.	anti-cell death gene; apoptosis; viral infection; inflammatory response	BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;		Amino acid sequence of human.		02-JAN-2001 (first entry)		AAB08843;		AAB08843 standard; peptide; 184 AA.	ET 1

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B
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AAY94001
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is a necrosis factor (NF) kB activator. The method of the invention is

used to identify compounds which modulate BCMA activity (and thus NF-kB

activity). The specification describes a method of identifying a

polypeptide which increases gene expression from a promoter. The method

involves contacting a library of with a cell which expresses a

recombinant anti-cell death gene and a reporter gene operably linked to

the promoter, and then determining whether the expression of the

reporter gene is altered as a result of contact with library. The method

is useful for identifying polypeptides which increase or decrease gene

expression from a promoter. The BCMA polypeptide or nucleic acid are

useful for preparing a pharmaceutical composition for treating cancer,

apoptosis, viral infections, inflammatory response, such as rheumatoid

arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                               ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic she pain; disease; inflammation; swelling; anaemia; septic she pain; disease; inflammation; swelling; anaemia; septic she pain; swelling; anaemia; anaemia; swelling; ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 32; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell degene and reporter gene, and determining alteration in reporter gene
                                                                                                                                         immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic insulin dependent diabetes mellitus; Crohn's disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                              Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY94001;
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                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 transmembrane activator and CAML-interactor; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY94001 standard; Protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dentifying compounds that modulate NF-kB expression and thus for drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                               occlusion; cholesterol;
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Pred. No. 1.3e-95;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal neoplasms, multiple myelones, lymphomas, light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or septic shock BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or anaegonists can be used to treat hypertension, renal artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAMI-interactor (TACI) receptor. TACI is a tumour necrosis factor (TACI), Taceptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TMF ligand. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an antibody production. The activated from a production is associated with an activated collected from a production is associated with an activated collected from a production is associated with an activated collected from a production is associated.
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                                                                                                   AAE09241 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA58559
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASYTNSVKGTNAILWTCL
                                                                                                                                                                                                                                                                             YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 152; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 1.3e-95;
Mismatches 0;
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19-NOV-2001 AAE09241;

(first entry)

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Best Local
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TWRF) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
            AAE00506 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-541628/60.
N-PSDB; AAD15902.
                                                                                                                                                                                                                                                                                                                                   Sequence
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22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                psoriasis.
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                                                                                                                                                                                          GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
                                                                                                                                                                                                                                                                                                                                                             protein.
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                                                                                                                                                   YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
                                                                           ISAR
                                                                                                                            YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) GENENTECH INC.
                                                                                                                                                                                                                                                                                  184;
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                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour necrosis factor; TALL-1; APRIL; TNF
BCMA; therapy; cancer; leukaemia; myeloma;
disease; rheumatoid arthritis; multiple scl
                                                                                                                                                                                                                                                                                 Conservative
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2000US-0226986
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                                                                                                                                                                                                                                                                              100.0%; Score 964; DB 22; 100.0%; Pred. No. 1.3e-95; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sclerosis;
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120 60

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MLQMAGQCSQNEYEDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILMTCL

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CC disease, renal disorders, B-cell lympho-proliferation, cardiovascular Cdiseases, renal disorders, B-cell lympho-prolifers, B-cell lympho-prolifers, B-cell lympho-prolifers, B-cell lympho-prolifers, B-cell lympho-proliferation, and disorders, B-cell lympho-proliferation such as cancer or CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, CC prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular CC diseases, renal disorders, B-cell lympho-proliferative disorders, CC lumunosuppressive diseases, organ transplantation, inflammation and CC human immunodeficiency virus (HIV), and for treating, suppressing or CC altering an immune response involving a signalling pathway between CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. CC The present sequence is human APRIL-R also referred as BCMA or CC BCM protein.
Qy
                                                  Query Match
Best Local
                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist
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                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carolnoma. The method involves administering a composition comprising a Proliferation Inducing Ligand Receptor (APRIL R) also referred as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOJ )
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2001
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                                                                                                  Sequence
 MIQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVINSVKGINAILWTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-266242/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOGEN INC.
APOTECH R & D
                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lung; colon; breast;
                                                                                                  184
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3A;
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2000US-0215688
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ng; colon; breast; prostate; Grave's disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        85pp; English.
                                                100.0%;
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                                   0
                                  Score 964; DB 22;
Pred. No. 1.3e-95;
Mismatches 0;
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RRESULT 5
AAB60698
AID AAB6
XX AAB6
XX AAB6
XX AAB6
XX AAB6
XX AAB6
XXY AUME
ACC AUME
XX HUME
KW HUME
KW B-CC

The invention relates to the use of a BAFF receptor (BAFF-R, also known CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory CC agent, and also plays a role in the development of hypertension and CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R, CC specific antibodies can be used for inhibiting B-cell growth dendritic CC cell-induced B-cell growth and maturation, and immunoglobulin production, CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative CC disorders, hypertension and renal disorders. The BAFF-R proteins may also CC be used in the treatment of immunosuppressive disorders and HIV confection, and in patients undergoing organ transplantation. The BAFF-R pecific antibodies may be used for treating, CC suppressing or altering an immune response involving a signalling pathway CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune-related disorder; B-cell growth inniutur, production inhibitor; immune-related disorder; B-cell immunoglobulin production inhibitor; B-cell maturation inhibitor; immunoglobulin production inhibitor; B-cell maturation altoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; autoimmune haemolytic anaemia; rapidly progressive glomerulonephritis; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF59998
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11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-2000; 2000WO-US22507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB60698
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2000US-0183536
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01-MAY-2000;
                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                              05-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                16-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              progressive glomerulonephritis, and lymphomas. Nucleic acids envisors BAFF-R may be used in gene therapy to treat tumours, lympl autoimmune disorders and inherited B-cell-associated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human B cell maturation factor (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibits B-cell growth and maturation it is useful for treating dise such as systemic lupus erythematosus, autoimmune haemolytic anaemia, crave's disease, multiple myeloma, B-cell carchomas, leukaemia, rap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY71979 standard;
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factor; pemphigus vulgaris; B-lymphocyte prolife
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Pred. No. 1.3e-95;
Mismatches 0;
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nephrotropic; hypotensive; gené therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft rejection; Crohn's disease.
                                                                                                                                                                                                                        Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in diagnostic assays.

The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by located on chromosome but not by brain, muscle, heart, lung, k1 pancreas, testis and placenta. BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocyte proliferation, used autoimmune disorders -
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Pred. No. 1.3e-95;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                         antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive CC activities, and can be used in gene therapy. (I) can be used for CC inhibiting, in a mammal, the activity of a ligand that binds Ithri? CC (e.g. INFA), for treating disorders and diseases associated with B CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for CC inhibiting the proliferation of tumour cells. (I) is useful for treating CC autoimmune disorders such as systemic lupus erythematosus, myasthenia CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid CC leukaemia, nephritis, and pyelonephritis, and for treating renal CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or CC amyloidosis, hypertension, large vessel diseases, graft-versus host CC disease, graft rejection and Crohn's disease, (I) is useful for CC disease, graft rejection and Crohn's disease. (I) is useful for CC development, for modulating the immune system, for regulating B cell responses and CC communication. The present sequence represents a protein which is CC given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                 Query Match
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28-JUN-2001;
29-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 designated Ztnfrl2 (I). (I) has cytostatic, immunosuppressive, dermatological, antinflammatory, neuroprotective, antidiabetic,
                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes a human tumour necrosis factor spated Ztnfr12 (I) (I) has cytostatic, immunosuppressive,
                                                             GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
                                                                                                                                              GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
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ISAR 184
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                              ISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated human tumor necrosis factor receptor polypeptide, 12, useful for treating autoimmune disorders, emphysema, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       renal failure or renal disease and lymphoma
                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                   184 AA;
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                                                                                                                                                                                                                                                                  Conservative
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2000US-257131P.
2001US-301715P.
2001US-315565P.
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Pred. No. 1.3e-95;
                                                                                                                                                                                                                                                                  Mismatches
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RESULT

Query Match Best Local Similarity

98.5%;

Score 950; Pred. No.

4e-94; DB

Length 181;

0

Gaps

0

60 63

180 183 120

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AAE15484
ID AAE1
                                                                               CC protein (BCMA) activity in a mammal. The method comprises administering CC a specific binding partner for ARRIL (370, a tumour necrosis factor TNF CC family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region CC of TACI or BCMA. The method is useful for inhibiting activity of TACI CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell CC lymphoproliferative disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI CC antagonists are useful for treating inflammation and immune function CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC diseases, optication of the series (asthma, hypersensitivity lung CC disease), drug and insect sting allergy, inflammatory bowel disease (CC conn's disease, colitis), scieroderma, autoimmune disease (multiple scierosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leurocyte infilitration of the autor of the series of the content of the series of the content of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                          activator and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 10A;
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14-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family ligand
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                                           leucocyte infiltration of uman BCMA protein.
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; 2000US-214591P.
; 2001US-0214591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to a method for inhibiting TACI (transmembrane intracellular CAML interactor) and/or B cell maturation
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is specifically claimed
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                                                             organs. The present
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Sequence

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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory

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This is region in claim 1 of
RESULT 9
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B-cell maturation inhibitor; immunoglobulin production inhibitor;
autoimmune disorder; B-cell lymphoprolliferative disorder; hypertension
renal disorder; immunosuppressive disorder; HIV infection;
organ transplantation; antiinflammatory; systemic lupus crythematosus;
autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                        Example 1; Fig
                                                                                           Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                                                                           N-PSDB;
                                                                                                                                                                              nompson
                                                                                                                                                                                                               (BIOJ )
                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                            17-AUG-1999;
11-FEB-2000;
                                                                                                                                                                                                                                                                                                16-AUG-2000;
                                                                                                                                                                                                                                                                                                                       22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                              WO200112812-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BAFF-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60700
                                                                                                                                                                                                                                                   18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                           Lymphoma; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB60700 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILYTTKTNDYCKSLPAALSATEIEKSISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASYTNSVKGTNAILWTCLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIISLAVFYLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                           AAF60000
                                                                                                                                                                                                               APOTECH
                                                                                                                                                                                                                           BIOGEN
                                                                                                                                                                              ü
                                                                                homolog
                                                                                                                                                                                       Browning
                                                                                                                                                                                                                                                 99US-0149378.
2000US-0181684.
2000US-0183536.
                                                                                                                                                                                                                                                                                                2000WO-US22507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAFF receptor; TNF family; immunoregulatory d disorder; B-cell growth inhibitor; BCMA;
                                                        u
                                                                                                                                                                                                                                                                                                                                                                                          therapy; cancer; tumour; plasmid pJST535.
                                                                                                                                                                                                              R & D
                                                        59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 157
                                                                                                                                                                                        Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAFF-R)
                                                                                                                                                                                                               SA.
                                                        English
                                                                                                                                                                                        Ambrose C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence encoded by A plasmid
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                                                                                                                                                                                        Schneider
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agent;
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pJST535

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RESULT 10
AAB08844
ID AAB08
XX AAB08
AC AAB08
XX DT 02-JA
XX ECAL
XX E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-C CC specific antibodies can be used for inhibiting B-cell growth, dendritic CC cell-induced B-cell growth and maturation, and immunoglobulin production, CC and in the treatment of autoimmune disorders. He cell lymphoproliferative C disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV CC infection, and in patients undergoing organ transplantation. The BAFF-R CC proteins or BAFF-R specific antibodies may be used for treating, an immune response involving a signaling pathway compared to the state of the second state of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-cell death gene;
rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory resp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of murine BCMA polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB08844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB08844 standard; peptide; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                            24-FEB-1999;
                                                                                                                                                24-FEB-2000; 2000WO-US04925
                                                                                                                                                                                                                                                                                                 WO200050633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agent, and also plays a role in the development of hypertension and
(GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISAR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLSLIIS---FVLMFLLRKISSEPLKD---NTGSGLLGMANIDLEKS---DEIILPRGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTVEECT --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
157; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shorter than that given in AAB60698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                            99US-0121485
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                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 47..72
                                                                                                                                                                                                                                                                                                                                                                          /note-
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85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                          "putative transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157;
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RESULT 11
AAX711980
ID 71807
AC AAX71
AC AAX71
AC AAX71
XX 28-MA
DT 28-MA
XX Murin
KW Murin
KW Tumou
KW Tumou
KW Thera
KW Syste
KW Haemo
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KW B cell
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KW B cell
KW B cell
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XX Mus m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC The present sequence represents a BCMA (not defined) polypeptide. BCMA
CC is a necrosis factor (NF) kB activator. The method of the invention is
CC used to identify compounds which modulate BCMA activity (and thus NF kB
CC activity). The specification describes a method of identifying a
CC polypeptide which increases gene expression from a promoter. The method
CC involves contacting a library of with a cell which expresses a
CC recombinant anti-cell death gene and a reporter gene operably linked to
CC the promoter, and then determining whether the expression of the
CC reporter gene is altered as a result of contact with library. The method
CC is useful for identifying polypeptides which increase or decrease gene
CC expression from a promoter. The BCMA polypeptide or nucleic acid are
CC useful for preparing a pharmaceutical composition for treating cancer,
CC apoptosis, viral infections, inflammatory response, such as rheumatoid
CC identifying compounds that modulate NF-kB expression and thus for drug
CC designing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 117; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell due gene and reporter gene, and determining alteration in reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed
                                                                                                                                  Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; Therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 32; Fig 7B; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                         Murine
                                                                                                                                                                                                                                                                               28-MAR-2001
                                                                                                                                                                                                                                                                                                                     AAY71980;
                                                                                                                                                                                                                                                                                                                                                          AAY71980 standard; Protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 designing.
                                                                                                                   thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 EKPTHTR 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-558405/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt LVLSLALETISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT
                                                                                                                                                                                                                                    B cell maturation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
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                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.3%;
62.6%;
                                                                                                                                                                                                                                    factor (BCMA) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 572; DB 21;
Pred. No. 2.1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 185;
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an anti-cell death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178
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haemolytic anaemia; Grave's disease; myasthenia gravis; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte pr

proliferation,

glomerulonephritis;

post-streptococcal

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RESULT 12
AAE15490
ID AAE15
XX
AC AAE15
XX
DT 12-MA
XX
DE Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to Tumour necrosis factor (TNF) and CC Apol-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid colored molecules, proteins (including homologues), and their antibodies. The CC invention in particular relates to methods for regulating the colored interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell cometuration factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying CC compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid cc arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes cautoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, CC The TALL-1 protein and its corresponding nucleic acid sequence are also cuseful in diamonatic namava
                                    12-MAR-2002
Mouse B cell maturation (BCMA) protein.
                                                                     AAE15490
                                                                                               AAE15490 standard; Protein; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocyte proliferation, used to identify compounds that regulate autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 37; Page 107-108; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in diagnostic assays.
                                                                                                                                                                                  179
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N-PSDB; AAD02130.
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01-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                    1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
                                                                                                                                                                                                                                                                                                                                                                                     4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASYTNSVKGTNAILWTCLGLS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is a murine B cell maturation factor (BCMA) A is the receptor for TALL-1 protein.
                                                                                                                                                                                                             EKSISAR
                                                                                                                                                                                                                                                                                                    LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL 118
                                                                                                                                                                                                                                                                                                                       LIISLAVFVLMFILRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                                                                                                                                                                EKPTHTR 185
                                                                                                                                                                                                                                       EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM 178
                                                                                                                                                                                                                                                                   EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                               184
                                (first entry)
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2000US-0201012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 572; DB 22;
Pred. No. 2.1e-53;
1; Mismatches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 185;
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80 PB

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                                                                                                                                                                                                                   The invention relates to a method for inhibiting TACI (transmembrane CC activator and intracellular CAML interactor) and/or B cell maturation extivator and intracellular CAML interactor) and/or B cell maturation CC protein (BCMA) activity in a mammal. The method comprises administering CC aspecific binding partner for APRIL (G70, a tumour necrosis factor-TNF CC family ligand), having the consensus region of TACI, BCMA, or the TACI/CC activation of the consensus sequence, but not the extracellular region CC and/or BCMA in a mammal which is useful for inhibiting activity of TACI CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell CC (treative disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI CC antagonists are useful for treating inflammation and immune function CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC disease, collitis), scheroderma, autoimmune disease (multiple Scherosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer country infilarration of the attin or cranse The present commence.
                                                                                                                                    Matches
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                        with leucocyte infiltration of the skin or organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 11; 94pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; panoreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
                                                                                                                                                                                                                                                           is mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theill LE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-2000; 2000US-204039P
27-JUN-2000; 2000US-214591P
14-MAY-2001; 2001US-0214591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family ligand
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           5
                                                                                                                                                     Local Similarity
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                                                                                            4
LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                              MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT
                                                                                   MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-066686/09
                                                                                                                                                                                                                                                    BCMA protein.
                                                                                                                                                                                                                 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arthritis; atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yu G;
                                                                                                                                  Conservative
                                                                                                                                                   59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                  21;
                                                                                                                                               Score 572; DB 23;
Pred. No. 2.1e-53;
                                                                                                                               Mismatches
                                                                                                                                                                   Length 185;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                      The present sequence
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                                                                                                                         Gaps
                                              58
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179 178

EKPTHTR 185 EKSISAR

184

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protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor TNF family 11gand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI on BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; collitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE15501;
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                                   (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple terosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucceyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region.
                                                                                                                                    antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crobn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human B cell maturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2002
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation (A_{\rm c})^2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theill LE,
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27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane activator and intracellular CAML interactor; TACI;
  58
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                   94pp; English.
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Query Match Best Local Similarity

33.5%;

Score 323; Pred. No.

DB 23; 3e-27;

Length

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RESULT 14
AAE15491
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                                                        The invention relates to a method for inhibiting TACI (transmembrane calcivator and intracellular CAML interactor) and/or B cell maturation correction (BCMA) activity in a mammal. The method comprises administering protein (BCMA) activity in a mammal. The method comprises administering calcivation (BCMA) activity in a mammal. The method comprises administering calcivity in a section of TACI, BCMA, or the TACI/ BCMA extracellular consensus region of TACI, BCMA, or the TACI/ BCMA extracellular consensus sequence, but not the extracellular region conformation of TACI or BCMA, in a mammal which is useful for treating activity of TACI cand/or BCMA, in a mammal which is useful for treating Bcell or T-cell cand/or BCMA in a mammal which is useful for treating Bcell or T-cell candyor BCMA in a mammal which is useful for treating Bcell or T-cell cantagonists are useful for treating inflammation and insume function continuous such as diarrhoea, psoriasis, allergies, pneumonia, atopic diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic constantitis, respiratory allergic disease (asthma, hypersensitivity lung consensus), fungal, seclesses, drug and insect sting allergy, inflammatory bowel disease (Conn's disease, colitis), scleroderma, autoimmune disease (multiple contensus), fungal, attractial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC
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27-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis; atherosclerosis; mouse
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                                      is human-murine B cell maturation protein (BCMA) consensus sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane activator and intracellular CAML interactor;
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2000US-214591P.
2001US-0214591.
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                                                                                                                                                                                                                                                                                                                                          Chimeric - Chimeric -
Treating a mammal for a condition associated with
                                WPI;
                                                                                                                                                                                                                                                                                                                                                                             B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; murine tumour necrosis factor; B cell maturation protein; BCMA; fusion prote
                    N-PSDB; AAD03847
                                                                                                                                        05-OCT-2000; 2000WO-US27579
                                                                                                                                                                                                                                                                                                                        Key
                                                  Schneider P,
                                                                      (APOT-)
                                                                                 (BIOJ
                                                                                                   30-JUN-2000;
                                                                                                             11-FEB-2000;
                                                                                                                      06-OCT-1999;
                                                                                                                                                             12-APR-2001
                                                                                                                                                                                 WO200124811-A1
                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                       Human; A Prollferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BCMA-Immunoglobulin G
                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE00507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE00507 standard; Protein;
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                                                                  BIOGEN INC.
APOTECH R & D SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96;
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2000US-0181807.
2000US-0215688.
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                                                                                                                                                                                                                     /note=
24..302
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                                                                                                                                                                                                                                                             /label= Mature_human_BCMA_IgG_Fc_fusion_protein 23..75
                                                                                                                                                                                                   /note-
                                                                                                                                                                                                             /label-
                                                                                                                                                                                                                                                                                         /label= Signal_peptide
/note= "Derived from m
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                                                                                                                                                                                                 "Derived from human BCMA"
                                                                                                                                                                                                                               "Derived
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                                                                                                                                                                                                                                                                                                                                                                    Fc region.
                                                                                                                                                                                                          Cysteine_rich_domain
                                                Cachero
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Pred. No. 1.3e
4; Mismatches
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                                                Ambrose
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7;
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                                                                                                                                                                                                                                                                                                                                                                                      TNF; murine;
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cell
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disenses, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HTV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is a fusion construct containing human APRIL-R also referred as BCMA or BCM protein, Fc region of human immunoglobul G (IGG) and a signal sequence from murine Ig kappa cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                     associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BEM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lugus erythematosus SLE); hypertension, cardiovascular itemates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3B; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to a method of treating
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GKEYKCKVSNKALPA-PIEKTIS
                                                        VT - -
                                                                                                                                  GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
                                                                              YTVEECTCEDCIKSKPKVDSD------HCFPLPAMEE-----GATILVTTKTNDY--
                                                                                                                                                               MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGVDK-THTC-
                                                                                                                                                                                                                          81;
                         -CKSLPAALSATEIEKSIS
                                                  -CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 170
                                                                                                                                                                                                                       Conservative
                                                                                                         -----PPC-----PAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                      Score 286.5; DB 22
Pred. No. 2.3e-22;
3; Mismatches 54;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                    Gaps
                                                                              164
                                                                                                                                                                81
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Query Match Best Local Matches

Similarity

29.7%;

DB 22;

Length

302;

Sequence

302 AA;

Search completed: November time 71.2833 secs 12, 2002, 16:58:31

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                              ## 1 App11
## 2 App11
## 3 App11
## 4 App11
## 3 3 App11
## 4 App11
## 3 3 App11
## 4 App1
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8, Appli
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12, Appl
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ADDRESSEE: Lyon & Lyon

633 West Fifth Street

7.1 8 7.1 8 7.1 11 7.1 11 7.1 11 7.1 11 7.1 12 7.1 12 7.1 12 7.1 12 7.1 13 7.1 13 7.1 13 7.1 13 7.1 3	SULT 1 -08-357-642A-1 Sequence 1, Apparent No. 583 GENERAL INFOR APPLICANT: APPLICANT: APPLICANT: TITLE OF IN TITLE OF IN TUMBER OF S CORRESPONDE		45				41	40	39	38											
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-486-270-12 Sequence 12, -367-264-12 Sequence 12, -153-757-8 Sequence 8, -153-757-8 Sequence 8, -153-757-10 Sequence 10, -367-264-10 Sequence 10, -153-757-10 Sequence 10, -153-757-10 Sequence 10, -465-337A-18 Sequence 10, -465-837A-18 Sequence 11, -45-837-18 Sequence 11, -188-228-42 Sequence 22, -045-632-29 Sequence 22, -168-532-29 Sequence 22, -168-532-29 Sequence 22, -168-632-29 Sequence 23, -168-632-29 Sequence 24, -168-632-29 Sequence 24,	licatic 524 ATION: Sima Le Joseph ENTION: ENTION: QUENCES QUENCES		7.0		٠	٠	•	7.1	7.1	.1	-	L			<u>. </u>	7.1	7.1	7.1	7.1	7.1	
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; TYPE: amino acid
; STRANDEDNESS: sinc
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-08-357-642A-1
Query Match
Best Local Similarity
                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209//
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR
                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,
FILING DATE: December 15, 1994
                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: Calliornia
COUNTRY: U.S.A.
                                                                                                                       TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 5.1
                                                                                                                                          1009
                                                                  peptide
                                                                                                      single
 8.2%;
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Score 79.5;
Pred. No. 2
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               Length 1009;
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RESULT 3
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US-08-460-626-1
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                NAME: Watburg, Richard J. 77
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: December 15
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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TITLE OF INVENTION: METHOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                       306 RSIRCLPL---EEGQAVL 320
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                                                                                                                           88
                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                            TELEFAX: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
RMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/460,626 FILING DATE: June 2, 1995 CLASSIFICATION: 435
                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM CON
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                 DSDHCFPLPAMEEGATIL 156
                                                                                        KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
                                                                                                                    EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
                                                                                                                                                                 Similarity
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633 West Fifth Street
                                                                                                                                                       Conservative
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Pred. No. 2.5;
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; Sequence 2, Application US/09290333 ; Patent No. 6316222 ; GENERAL INFORMATION:
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US-09-290-333-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: N
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPI
TITLE OF INVENTION: CAML, I
TITLE OF INVENTION: THEREO
NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                        140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                                                                                   152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
                                                                                                                     210 QDH----
                                                                                                                                                                                                                          108 --- RTGDEIILPRG---
                                                                                                                                                                                                                                                             93
                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                        34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Ha
                                                                                                                                                                                                                                                                                                                                                       8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                     I-----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                       CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
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19.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26,742
26,742
PER: 1340-1-007
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                                                                                                                       230
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                   Sequence 2, Application US/08179481
Patent NO. 5624816
GENERAL INFORMATION:
APPLICANT: CARRAWAY, KERMIT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT:
                                                                                                                                                                                                    210 QDH-----AMEAGSPVSTSPEPVETC 230
                                                                                                                                                                                                                                         140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                                                                                                                                                                                 152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
                                                                                                                                                                                                                                                                                                                                                              93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEYENNSDNSGR-YQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-199
CLASSIFICATION: cUnknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                           ---RTGDEIILPRG----
                                                                                                                                                                                                                                                                                                                                                                                                      I-----SLAVFVLMFL------LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 293 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: David A. Jackson, Esq.
             CARRAWAY, KERMIT L.
CAROTHERS CARRAWAY, CORALIE
FREGIEN, NEVIS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                von Bulow, Gotz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 78.5; DB
19.9%; Pred. No. 0.56;
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US-07-717-331F-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At The Self-Incompatability |
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
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ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,481
                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                        167
                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 EDLPVFNATGVLLIQNGSQVSANFDGTVTISVIALSNILHASSS--LSEEYRNHTKGLLG
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TYPE: amino acid
11near
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                       ZIP:
                                                       COUNTRY:
                                                                           STATE:
                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                          99 MANIDLEKSRTGDEIILPRGLEYTVEECTCEDCI 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 LEGRTAQTDSANATNETAFAAQYNTSSLKSPITVQWFLEPNDTIRVVHNNQTVAFNTSDT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC-----NASVTNSVKGT 52
                                                                                                                                                                                                                                                                                                                                                                                      VWNDNPE-----DDFRMPNG--STIPSNTSEETL 193
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                                                                       Connecticut
                                                                                                         25 Skytop Drive
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                                                         USA
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                                                                                                                            Yahwak & Associates
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                                                                                                                                                                              A Receptor Protein Kinase Gene
Encoded At The Self-Incompatab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.9%; Score 76; DB 1; Length 744;
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                                                                                                                                                                                  Self-Incompatability Locus
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US-09-232-160-18
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, MOLECULE TYPE: peptide
US-07-717-331F-2
                                                                                                                                                                                                                                                 APPLICANT: Steve Daniel
APPLICANT: James Gilmore
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Laura Stuve
TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: PA-0003 US
CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT FILLING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL PROGRAM
SEQ ID NO 18
                                                                                                       Best
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09232160 Patent No. 6368794
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Best Local :
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TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE: -
                                                                                                                                                                               OTHER INFORMATION: 1299627
                                                                                                                                                                                                                                           TYPE: PRT
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LENGTH: 857 amino acids
TYPE: amino acid
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FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 FSSCNKL 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCF----PLPAMEEGATILVTTKT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 ADIAKKRNASGKIISLTVGVSVLLLLIMFCL-----WKRKQKRAKASAISIANTQRNQ 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 CKKRCISD---CNCTAFANADIRNG--GSGCVIWTERLEDIRNYATDAIDGQDLYVRLAA 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 NLPMNEMVL----
                                   13 YFDSLLHAC-IPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLG----LSLIIS 67
          23
                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 ------CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 CQLRCSSNTPPLTCQRYCNASYTNSVKGTNAILWT-------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 7.8%; Score 75; DB 1; Length 857;
Local Similarity 17.6%; Pred. No. 6.6;
hes 33; Conservative 30; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: George M. Yahwak REGISTRATION NUMBER: 2
YADDCLAQCGKDCKSYCCDGTTPYCCSYY--AYIGNILSGT-AIAGIVFGIVFIMGVIAG 79
                                                                                                   Similarity
                                                                                Conservative
                                                                                                     25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/07/717,331F
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                                                                                16;
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                                                                                            Score 70.5; D
Pred. No. 1.9;
                                                                              Mismatches
                                                                                                               DB 4;
                                                                              52;
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                                                                                                                 Length 154;
                                                                            Indels
                                                                          21;
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                                                                        Gaps
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US-09-290-333-6
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Best Local Similarity
"-+ches 15; Conserva
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                                                                                    Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/810, FILING DATE: 28-FEB-1997 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1340-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: PHYPOTHETICAL: NC FRAGMENT TYPE: NC ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bram, Richard J.

APPLICANT: von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        34 CPEEOYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                        8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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VON BULOW, GOTZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
                                                                     APPLICANT: Bram,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEEC
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5, 5969102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 amino acids

    David A. Jackson, Esq.
    Hackensack Ave, Continental Plaza, 4th

                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal
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                                                                                                                                                                                                                                                                                              7.2%;
                                                                     Richard J.
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                                                                                                                                                                                                                                                                           Score 69.5; DB Pred. No. 2.8; 14; Mismatches
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Patent No. (
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                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                  CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                 APPLICANT: Sharp, Robert L.
APPLICANT: Snyder, Yvonne M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN
TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                                                            APPLICANT:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1340-1-007 PCT TELECOMMUNICATION INFORMATION:
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ADDRESSEE: David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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                                                                                                            rRY: United States of America
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                                                                                                                                                 Indianapolis
Indiana
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                          Mayne,
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411 Hackensack Ave, Continental Plaza, 4th
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                  #1.25
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RESULT 11
US-08-660-148-5
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APPLICANT: Burnett
APPLICANT: Mayne,
APPLICANT: Sharp,
APPLICANT: Snyder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5,
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Best Local
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1180 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Gaylo, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Snyder, Yvonne M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
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                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gaylo, Paul J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                   CLASSIFICATION:
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: X-9419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CSQNEY-FDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGIN-----AILWTCLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGI------CLGYLCTFCLIAKPK--QIYCYLQRIGIGLSPAMSYSALV---TKTNRIAR 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSLIISLAVFVLMFLLR-----KISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILP 116
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                                                                                                                                                                                          46285
                                                                                                                                                                                                                                        Indianapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08660148
                                                                                                                                                                                                                         Indiana
                                                                                                                                                                                                                                                           E: Eli Lilly and Company
Lilly Corporate Center
                                                                                                                                                                                                         United States of America
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                                                                                                                                                                                                                                                                                                                                                                                    Sharp, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                     Burnett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                   Nancy G.
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24.68;
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 US/08/282,853
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Pred. No. 4
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               TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Huang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (317) 276-3861 INFORMATION FOR SEQ ID NO: 5:
                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE,DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 06-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive,
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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LENGTH: 1212 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       537 CKENEYVEDE--YTCKACQLG-SWPTDDLT---GCDLIPVQYLRWGDPEPIAAVVFACLG 590
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                                                                                                                                                                                                               FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Diego
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/459,568
                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CSONEY-FOSLLHACIPCOLRCSSNTPPL/TCORYCNASVTNSVKGTN-----AILWTCLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------DYCKSLPAALSA 174
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Pred. No. 47;
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TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-459-568-2
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US-08-399-411-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: ns /ns /190 /11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino aci
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                            598 PVTVE-----ITQNIKSTQV------626
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                     94
                                                                              34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG 93
                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-1
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SGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLP 147
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                 1706 amino acids
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                              7.2%; Score 69.5; [
21.7%; Pred. No. 77;
tive 22; Mismatches
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21.7%; Pred. No. 77;
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RESULT 15
US-09-586-472-2
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                                                                                                                                                                               598
                                                                                                                        148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
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SOFTWARE: PatentI
                                                                                                                                                                                             94
                                                                                                                                                                                                                                                             34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P-LJ 1776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 01
FILING DATE: 06-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                           SGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLP 147
                                                                                                                                                                                                                               PVTVE-----ITQNIKSTQV------626
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                                                                                                                                                            -----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLSLPLSISTAEVVSFH-----
                                                                                       -KEKG--VYLSSKLKQLLQTQDKLTLPAGFSAAEIPK 708
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                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (619)
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang, Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535-8949
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21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/292,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/399,411
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Village Drive,
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Pred. No. 77;
                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                 DB 3;
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Search completed: November 12, Job time: 28.2704 secs
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GENERAL INFORMATION:
APPLICANT: Huang,
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                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                           148 AMEEGATILYTTKTNDYCK----SLPAALSATEIEK 179
                                                                                                                                                                                                                        598 PYTYE-----ITQNIKSTQV----
                                                                                                                                                                                   94 SGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLP 147
                                                                                                                                                                                                                                                            34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG 93
                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Retinoblastoma Protein - Interacting
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                      -KEKG--VYLSSKLKOLLOTODKLTLPAGFSAAEIPK
                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/586,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1706 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/292,683 FILING DATE: 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/528,706 FILING DATE: 17-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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Listing first 45 summaries
                /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

NO.	score	Match Length		B	Ω	Description
	950	98.5	181	10	US-09-854-864-5	Sequence 5, Appli
2	572	59.3	185	10	US-09-854-864-11	Sequence 11, App.
(L)	323	33.5	58	10	US-09-854-864-21	Sequence 21, Appl
4	311.5	32.3	117	10	US-09-854-864-12	12,
Ç	286	29.7	283	10	US-09-854-864-9	Sequence 9, Appli
6	284	29.5	51	10	US-09-854-864-6	Sequence 6, Appli
7	201	20.9	34	10	US-09-854-864-7	Sequence 7, Appli
8	201	20.9	81	10	US-09-854-864-13	Sequence 13, Appl
9	187	19.4	281	10	US-09-854-864-10	10,
10	104	10.8	21	10	US-09-854-864-8	8
11	79.5	8.2	293	9	US-09-779-050A-42	
12	79.5	8.2	1009	œ	US-08-987-689A-2	Sequence 2, Appli
13	78.5	8.1	293	10	US-09-879-919-22	N
14	78.5	8.1	293	10	US-09-854-864-14	Sequence 14, Appl
15	78.5	8.1	293	10	US-09-961-376-2	Sequence 2, Appli
16	78	8.1	291	ဖ	US-09-779-050A-43	•
17	70.5	7.3	397	10	US-09-854-864-18	Sequence 18, Appl
18	70.5	7.3	1203	12	US-10-027-923-5	
10	70	7.3	180	10	115-09-780-717-11	=======================================

Sequence 2, Appli	9 US-09-886-429-2	418	6.7	64.5	5
Sequenc	10 US-09-224-683-44	195	6.7	64.5	44
Sequence	_		6.7	64.5	3
Sequence	12 US-10-105-929-6	-	6.7	65	42
Sequence	12 US-10-039-785-4		6.7	65	41
Sequence	10 US-09-737-149-30		6.8 3	65.5	40
Sequence			6.8 3	65.5	39
Sequence			6.8	65.5	38
Sequence	10 US-09-908-322-2	728	6.8	65.5	37
Sequence	10 US-09-735-787-4	376		66	36
Sequence	10 US-09-844-908-1	317		66	S
Sequence	9 US-09-844-988-1	317		66	34
Sequence 16, App.	10 US-09-854-864-16			66.5	33
Sequence 3				67	32
Sequence 8,	10 US-09-797-481-8			67	31
Sequence 2,	10 US-09-780-525-2			67.5	30
Sequence 45,	9 US-09-779-050A-45	37		67.5	29
Sequence	_	305	7.1	68.5	28
Sequence				69	27
Sequence	10 US-09-815-837-74			69	26
Sequence	10 US-09-797-481-7			69	25
Sequence	12 US-10-027-923-4			69.5	24
Sequence	10 US-09-854-864-15			69.5	23
Sequence	10 US-09-854-864-20			69.5	22
Sequence	10 US-09-925-301-1088	836	7.3	70	21
Sequence	10 US-09-780-717-44	182	7.3	0/	0.7

ALIGNMENTS

US-09-854-864-5

GENERAL INFORMATION:

Sequence 5, Application US/09854864 Patent No. US20020081296A1

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LENGTH: 181
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CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: THEILL, LARS EXDE APPLICANT: YU, GANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
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184 R 184
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                                                                                                                                                                                                                                                                                                                        LIISLAYFYLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV
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                                             ; ORGANISM: Homo sapiens US-09-854-864-21
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US-09-854-864-21
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 58
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  Query Match
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Best Local Similarity
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                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR EILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
FILE REFERENCE: A-686B
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
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                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILYTTKTNDYCK-SLPAAL-SATEI 177
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  33.58;
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  Score 323;
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                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENCTH: 283
TYPE: PRT
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
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Best Local Similarity
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                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI FILE REFERENCE: A-686B CURRENT APPLICATION NUMBER: US/09/854,864 CURRENT FILLING DATE: 2001-09-11 PRIOR APPLICATION NUMBER: US 60/204,039
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                                                                                               NUMBER OF SEQ ID NOS: 31
                                                                                                                  PRIOR APPLICATION NUMBER: US 60/214,591 PRIOR FILING DATE: 2000-06-27
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ORGANISM: Homo sapiens
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TYPE: PRT
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US20020081296A1
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Pred. No. 7.5e-25;
4; Mismatches 7;
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Patent No. US20020081296A1
GENERAL INFORMATION:
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                                                                                           APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
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CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
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TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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                                                                           NUMBER OF SEQ ID NOS: 31
                                       SOFTWARE: PatentIn version 3.1
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hes 51; Conser
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37.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.5%; Score 284; DB 10; 100.0%; Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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Pred. No. 8.8e-22;
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                                                                                                               ; ORGANISM: Mus
US-09-854-864-10
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LENGTH: 81
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Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
FILE REFERENCE: A-686B
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PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
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   187; DB 10;
No. 9.8e-12;
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; ORGANISM: Homo sapiens US-09-779-050A-42
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US-09-854-864-8
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US-09-854-864-8
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
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                                                                                                                                                                                                                                                                                      Sequence 42, Application US/09779050A Patent No. US20020160416A1
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                                                                     SEQ ID NO 42
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Best Local
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APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
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PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
                                                                                     NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
                                                                                                                        CURRENT APPLICATION NUMBER: US/09/779,050A CURRENT FILING DATE: 2001-02-12 PRIOR APPLICATION NUMBER: 60/181,800 PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/854,864 CURRENT FILING DATE: 2001-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI FILE REFERENCE: A-586B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
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                                  TYPE: PRT
                                                  LENGTH: 293
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Query Match
Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                         FILING DATE: June 2, 199
APPLICATION NUMBER: 08/3
FILING DATE: December 15
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                         TOPOLOGY: I MOLECULE TYPE:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: PYK2 RELATED PRODUCTS AND METHODS
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                                                                                                                                                                                                                                                NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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December 9, 1997
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US-09-879-919-22
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                                                                                                                             US-09-854-864-14
                                                             Sequence 14, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
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LENGTH: 293
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SOFTWARE: Patentin Ver. :
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PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/241,952
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PRIOR FILING DATE: 2001-03-33
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
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CURRENT FILING DATE: 2001-06-14
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TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P1
                          APPLICANT: THEILL, APPLICANT: YU, GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/016,812
PRIOR FILING DATE: 1996-03-14
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PRIOR EILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 08/815,783
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                    210 QDH-----AMEAGSPVSTSPEPVETC 230
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19.9%; Pred. No. 1
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PRIOR APPLICATION NUMBER: 60/254,874
PRIOR FILING DATE: 2000-12-13
PRIOR ADDITORMON
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CURRENT FILING DATE: 2001-09-11
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                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/533,822
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/188,208
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEO ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/961,376
CURRENT FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ruben et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
FILE REFERENCE: PF524P1
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PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
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PRIOR FILING DATE: 2000-09-26
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N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: HOmo sapicons (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: $43486; $31208; $36661
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S43486
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A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is A;Reference number: S43486; MUID:94218235; PMID:8165126
A;Accession: S43486
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ALIGNMENTS

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Minimum DB

Sequence:

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Maximum DB

Database

A;Residues: 1-184 <LAA>
A;Residues: 1-184 <LAA>
A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245
R;Laabi Y; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsap
EMBO J. 11, 3897-3904, 1992
A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208 A;Cross-references: GDB:135977; OMIM:109545 A;Map position: 16p13.1-16p13.1 A;Introns: 44/1; 93/1 C;Superfamily: human B-cell maturation factor A;Cross-references: EMBL:214954; NID:g29407; PIDN:CAA78679.1; PID:g29408 A;Accession: S36661 C; Genetics: A; Molecule type: mRNA A; Residues: 4-184 <LA3> A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-184 <LA2> A; Gene: GDB: BCMA A; Cross-references: EMBL: Z14955 Query Match Best Local Similarity Matches 121 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180 μ 1 MLQMAGOCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60 184; Conservative 100.0%; Score 964; DB 2; 100.0%; Pred. No. 5.6e-81; 0; Mismatches Length 184; 0 Gaps o,

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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: C97344
                                                                                                                                                                                                                                                                R; Weigmann, A.; Corbeil, D.; Hellwig, A.; Huttner, W.B. Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A; Title: Prominin, a novel microvilli-specific polytopic A; Reference number: 216512; MUID:98024147; PMID:9356465
A; Accession: T08881
                                                                                                                                                                                                                                                                                                                                                     prominin - mouse
C:Species: Mus susculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
C:Accession: T08881
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C;Superfamily: histidine permease protein M
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A; Residues: 1-217 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 14-Sep-2001 *sequence_revision 14-Sep-2001 *text_change 30-Sep-2001 C;Accession: C97344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid ABC transporter, permease component CAC3619 [imported] - Clostridium C_7Species: Clostridium acetobutylicum
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                                                                                                                                                                                           A;Cross-references: EMBL:AF026269; NID:g2559003;
                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                               A; Status: preliminary; translated
                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 ALGLTYGQTMKRIILPQAIRVVIPPCGNEFIAMIKDTSLVSVITMEELLRKAQLLVSSSG
                                                    18 LHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 SLLHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                         Local Similarity
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                    LVGCFFCMCRC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLIISLAVEV--LMFLLRKISSEPLKDEF----KNTGS-----GLLGMANIDLEKSR 108
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                                                                                                                                                                                                               1-858 <WEI>
                                                                                          44;
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                                                                                        Conservative
                                                                                                      9.0%;
                                                                                                                                                            membrane protein
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                  ---CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
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                                                                                      30;
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                                                                                      Score 86.5; D
Pred. No. 6;
30; Mismatches
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Pred. No. 0.98
25; Mismatches
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                                                                                                                        DB 2;
                                                                                                                                                                                            PIDN:AAB86715.1; PID:g2559004
                                                                                        67;
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ATCC824
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                                                                                        53;
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                                                                                     Gaps
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Best Local Similarity
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A;Status: process.
A;Molecule type: mRNA
A;Residues: 1-1009 <SAS>
A;Residues: 1-1009 <SAS>
A;Cross-references: GB:D45B54; NID:g1000679; PIDN:BAA08290.1; PID:d1008885; A;Cross-references: GB:D45B54; NID:g1000679; PIDN:BAA08290.1; PID:d1008885; C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein ly: unassigned Ser/Thr or Tyr-specific protein kinases
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;423-686/Domain: protein kinase homology <KIN>
F:423-439/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                           R;Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-t A;Reference number: A57434; MUID:95403356; PMID:7673154
A;Accession: A57434
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T13009
                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine kinase (EC 2.7.1.112) CAK-beta
N;Alternate names: cell adhesion kinase-beta
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Feb-1996 *sequence_revision 08-Feb-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 3
A;Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; C;Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T24C20.80 - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) c;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Nov-1999 C;Accession: T13009
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A; Residues: 1-1998 <CHO>
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                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A57434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: ATSP: T24C20.80
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A; Accession: T13009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLIGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLPAM 149
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29.4%;
  8.5%;
26.9%;
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Pred. No. 27;
     Score 82;
Pred. No.
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DB
18;
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                            Length 1009;
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Science 282, 2012-2018, 1998
A.Title: Genome sequence of the nematode C. elegans: a platform for investigation A.Title: Genome sequence of the nematode C. elegans: a platform for investigation A.Title: Genome sequence of the nematode C. elegans: a platform for investigation A.Title: Genome with the nematode C. elegans: a platform for investigation A.Title: Genome with the nematode C. elegans: a platform for investigation A.Title: Genome with the nematode C. elegans: a platform for investigation A.Title: Genome with the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for investigation of the nematode C. elegans: a platform for inv
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J. Mol. Biol. 222, 835-841, 1991
A;Title: Cysteine residue periodicity is a conserved
A;Reference number: 20504; MUID:92106337; PMID:176:
A;Accession: T28669
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T28669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein RO8F11.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
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                                                                                                                                                        A; Map position: 5
C; Superfamily: myeloperoxidase; myeloperoxidase homology
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-773 <STO>
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A; Residues: 1-2233 <NIE>
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                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:chr_V;
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; anonymous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Genetic code: SGC5
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                                                                                                                                                                                                                                   A; Gene: R08F11.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YTVEECTC----EDCIKSKPKVDSDHCFPLPAMEEGATI-----LVTTKTN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     520 GSCYQKQ----
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                                                                       Local Similarity
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25.1%;
                                                                   8.4%;
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                                                                                                                                                                                                                                                                                                                                   PIDN:AAB54249.1; PID:g2088832;
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Pred. No. 45;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-22,'G',24-150 <SA2>
A;Cross-references: GB:D45853; NID:g1000676; PIDN:BAA08289.1; PID:d1008884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase
A;Reference number: A57434; MUID:95403356; PMID:7673154
A;Accession: B57434
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A:Residues: 1-22,'G','24-434,'L','436-1009 <SAS>
A:Residues: 1-22,'G','24-434,'L','436-1009 <SAS>
A:Cross-references: EMBL:U43522; NID:g1165218;
R:Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka,
J. Biol. Chem. 270, 21206-21219, 1995
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A; Accession: G02330
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Nature 376, 737-745, 1995
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C;Species: 10-Apr-1996 #sequence_revision 27-Feb-1997 #text_change 17-Nov-2000
C;Accession: $60248; 602330; B57434
R;Lev, S.; Moreno, H; Martinez, R.; Canoll, P.; Peles, E.; Musacchio, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - N.Alternate names: cell adhesion kinase-beta
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Best Local :
                                                                                                                                                                                        Matches
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                                                                                              249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
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                                                                                                                                          88 EFKNTGSGLLGMANIDLEKSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA-----TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCQLRCSSNTPPLTCQ-----RYCN----ASVTNSVKGTNAILWTCL---GLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
  RSIRCLPL - - - EEGQAVL
                                              DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martinez, R.; Canoll, P.; Peles, E.; Musacchio, J.M.; Plowman
                                                                                                                                                                                                            8.2%;
  320
                                                                                                                                                                                           9;
                                                                                                                                                                                                            Score 79.5;
Pred. No. 31;
                                                                                                                                                                                           Mismatches
                                                                                                                                          -TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not shown
                                                                                                                                                                                                                                      DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:AAC05330.1; PID:g1165219
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                                                                                                                                                                                                                                      Length 1009;
                                                                                                                                                                                           Indels
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fall armyworm

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N;Alternate names: p
C;Species: Spodopter
C;Date: 11-Jan-2000
C;Accession: T43351
R;Cleplik, M.; Klenk
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1299 <CIE>
A; Cross-references: EMBL: Z68888; NID: g1167859;
A; Cross-references: clone Sfurin 6; ovary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Cieplik, M.; Klenk, H. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-343 <BI
                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A64300; A; Accession: D64469
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                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
                                                                                                                                                                               12 EYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVF 71
                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                  EII------DSDHCF-PLPAMEEG 152
                                                                                                      VLMFL------LRKISS--EPLKDEFKNTGSGLLGMA-----NIDLEKSRTGD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKGTNAIL-W 57
DVLKEEYEKYPDKFLYIVGDAKKEEVLK-KAKIDKAKGLIATLPSDADNVFLTLTARELN 199
                                                                                                                                          DYFTALYESVI-----TITTTGYGDFTPKTFLGRTLTVVYLCVGVGIVMYLFSL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALHTAPSADAAPSVAVVTIAVCAAAVGLFITVLVVLQAHSPREKKTRKTSVRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCLGLS------LIISLAV------FVLMFLLRKISSEPLKDEFKNTGSGLLGMAN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDLEKSRTGDEIILPR-GLEYTVEECTCEDCIKSKPKVDSDH 142
                                                                     1AEFIVEGKFEEFVRLKKMKNKIKTLKDHYIICGYGRLGKVVGEKFIEENIPFIAIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VEYSR-----LPRTDVDFTV----LTSCTDQEGPVEYEH 1289
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                                                                                                                                                                                                                    Similarity
39; Conserv
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24.1%;
                                                                                                                                                                                                                                                                                       hypothetical protein s110993
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                                                                                                                                                                                                                    35;
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                                                                                                                                                                                                                                                 Score 78.5;
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Pred. No. 4(
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                                                                                                                                                                                                                  66;
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killer cell inhibitory receptor p91A precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #te:
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F:24-841/Product: Killer cell inhibitory receptor p91A #status
F:24-818,119-220,221-315,316-418,419-517,518-618/Domain: extrac
F:638-674/Domain: transmembrane #status predicted CIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; J. Blochem. 123, 358-368, 1998
A:Title: Genomic structures and chromosomal location of
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                                                                                                                                                                                                                                                                                                                                                                                               F;636-674/Domain:
F;675-765/Domain:
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C;Comment: This protein function
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742
                                  163 DYCKSLPAAL-SATEIEKSISAR 184
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                                                                                                                                                    650 AFILFLFILIFILLRRRHRGKFRKDVQKEK------DLQLSSGAEEPITRKGELQK 699
                                                                                                                                                                                                                                    598 AQNSSFYLLSSASAPVELTVSGPTETSTPPPT-
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                                                                         RPNPAAATQEESLYASVEDMQTEDGVELNSWTPPEED------PQGET-----
                                                                                                                                                                                           IISLAVFVLMFLL--RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRG----
                                                                                                                                                                                                                                                                      SQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSL 64
                                                                                                               1 Similarity
46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein function
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                           8.1%; Score 78; DB 22.7%; Pred. No. 35; tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as inhibitory cell-surface
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                                                                                                                                                                                                                                  -- MSMPLGGLHMYLKALIGVSV 649
                                                                                                                                                                                                                                                                                                               61;
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                                                                                                                                                                                                                                                                                                                                                 Length 841;
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R:Theologis, A.; Lunci, Conn, L.; Conway, A.L., Ching, M.K.; Conn, L.; Conway, A.L., Ching, M.K.; Conn, L.; Conway, A.L., Ching, M.K.; Conn, L.; Conway, A. Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, A. Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait: Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A. Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S. A. Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A. Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F16F4.10 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002 C;Accession: D86345
A;Cross-references:
C;Genetics:
                                                                             A; Molecule type: DNA
A; Residues: 1-738 <STO>
                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Hughes, B.; Huizar, L.
                                  GB:AE005172; NID:g8920639;
                                      PIDN:AAF81361.1;
                                                                                                                                                                                                                                                                                                                                                      Southwick, A.M.; Sun,
                                      GSPDB:GN00141
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.S.; Malti, R.;
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Kim,

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A:Cross-references: EMBL:AL132956
A:Experimental source: cultivar Columbia; BAC C:Genetics:
A; Map position: 3
A; Introns: 69/3; 271/3;
A; Note: F2K15.50
                                                                                                                                                                                                                                                                                hypothetical protein F2K15.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000
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A; Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3; 806/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191152
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: The sequence of A. thaliana IG002N01
A;Reference number: Z14407
A;Accession: T01733
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C; Accession: T01733
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C; Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25;
                                                                                                                    A; Molecule type: DNA
A; Residues: 1-522 < RIE>
                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                               A; Reference number: Z23015
A; Accession: T45824
                                                                                                                                                                                                                       R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; submitted to the Protein Sequence Database,
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A; Residues: 1-968 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Scheet, P.; Maggi, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein A_IG002N01.31 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: A_IG002N01.31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 SLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSQNEYFDSLL-HACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLII 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAMEEGATILVTTKTND----YCKSLPAALSATEIEKSISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPL 146
                                                                                                                                                                                                                                                                                                                                                                                                                               --VPEPETVAATTTTVDKPVPEPEPVPEPVPVPAIEAAVAAQ 912
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                   294/1; 327/3;
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5; Mismatches
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                   397/3; 443/3
                                                                                                                                                                                                                       Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, January 2000
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                                                                               clone F2K15
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C:Superfamily: methyl-accepting chemotaxis protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Evidence for lateral gene transfer between Archaea A; Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methyl-accepting chemotaxis protein - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: F72288
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                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-539 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                          42 NASYTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD---EFKNTGSGLLG 98
                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                99 MANIDLEKSRTGDEI 113
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                                                                                                                                                      NVSMTKNIK-RNIIFF----LVVVCAAAMFIAIFTTRNLTT-PLKKLAVLVENLSHGVL- 202
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                    2002,
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      Score
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Gapop 10.0 ,
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Listing first 45 summaries
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YO78_TRICPP
Y077_RICPP
Y077_RICPP
Y077_RICPP
Y077_RICPP
Y078_PAPP
Y075_RAT
YCK5_MOUSE
G156_PARP
HS70_TRIRU
TLPC_BACSU
MGR5_HUMAN
ZAN_HOUSE
C5AR_RAT
PANE_YEAST
GC1M_MOUSE
R23B_MOUSE
R23B_MOUSE
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PROM_MOUSE
FAK2_MOUSE
FAK2_RAT
FAK2_HUMAN
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YD57, METJA
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TI3X_MOUSE
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094840 mus musculu
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0951867 bos taurus
09673 homo sapien
054990 mus musculu
099409 m protein t
074980 rattus norv
014836 homo sapien
058752 methanococc
09et35 mus musculu
074910 schizosacch
099092 brassica ol
041771 kluyveromyc
082295 drosophila
010331 ordyia pesa
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019324 tattus norv
08295 drosophila
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09pr43 urgaplasma
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09pr43 peramecium
093866 trichophyto
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098787 saccharomyc
001869 mus musculu
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SEQUENCE FROM N.A. KEDLINE-99425270; PubMer Loftus B.J. Kim UJ., Fuhrmann J., Mason T., Desilattes Mays A., Cao o Eichler E.E., Harris P., "Genome duplications and human chromosome 16p and human chromosome 18p and House FROM N.A., AND MEDLINE-21419161; PubMer Arbritis "; Genes Immun. 2:276-279(FUNCTION. MEDLINE-20363816; PubMer Hatzoglou A., Roussel J Inoue J., Devergne O., "TNF receptor family mea TNF receptor associated activates NF-Kappa B, e TRF receptor associated	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANS TISSUE-Peripheral blood leukocytes, and I MEDLINE-93010984; PubMed-1395683; Laabi Y., Gras M.P., Carbonnel F., Brouel Larsen C.J., Tsapis A.; "A new gene, BCM, on chromosome 16 is fus by a t(4;16)(q26;p13) translocation in a EMBO J. 11:3897-3904(1992). [2] SEQUENCE FROM N.A. MEDLINE-94218235; PubMed-8165126; MEDLINE-94218235; PubMed-8165126; Tabbi Y., Gras M.P., Brouet J.C., Berger "The BCMA gene, preferentially expressed maturation, is bidirectionally transcribe Nucleic Acids Res. 22:1147-1154(1994). [3]	TRIT_HUMAN STANDARD; TRIT_HUMAN STANDARD; Q02223; 01-JUL-1993 (Rel. 26, Cre. 01-JUL-1993 (Rel. 26, Las. 15-JUN-2002 (Rel. 41, Las. Thumor necrosis factor recomaturation protein). TWERSFIT OR BCMA OR BCM. HOMO Sapiens (Human). Eukaryota; wetazoa; Chord. Mammalia; Eutheria; Prima NCBL_TaxID-9606;	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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mitogen-activated protein kinase."; J. Immunol. 165:1322-1330(2000).

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Boyle W.J., Sarosi i., ....

"APRIL and TALL-I and receptors

humoral immunity.";

Mar Immunol. 1:252-256(2000).
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Madden K., Xu W., Parrish-Novak J., Foster D., Loft
Moore M., Littau A., Grossman A., Haugen H., Foley
Harrison K., Kindsvogel W., Clegg C.H.;
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Gross J.A., Johnston J., Mudri S., I
Madden K., Xu W., Parrish-Novak J.,
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REPEAT
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EMBL; Z29575; CAA82691.1; -.
EMBL; Z29574; CAA82690.1; -.
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SEQUENCE
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or send an email to license@isb-sib.ch).
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                                                                                                                                                 Transmembrane;
                                                                                                                                                             Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Promotes B-cell survival and plays a role in the regulation humoral immunity. Activates NF-kappa-B and JNK.

SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF1, and periluclear Golgi-like structures.

TISSUE SPECIFICITY: Expressed in mature B-cells, hereard, cells or monocytes.
                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T WHICH INVOLVES BCMA AND IL2.
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   RA Kawai J. Shinagawa A. Shibata K. Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Oxido T., Frurno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustinnich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustinnich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRAIN-C57BL/6J; TISSUE-Colon;
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                                                                    Nature 409:685-690(2001)
                                                                                      "Functional annotation
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FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL. Promotes B-cell survival and plays a role in the regulation humoral immunity. Activates NF-kappa-B and JNK (By similarit SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF
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characterization of murine BOMA gene defines it as
he tumor necrosis factor receptor superfamily.";
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. No. 1.3e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae;
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                                                                                      collection.";
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                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Created)
16-JUN-2002 (Rel. 41, Last sequence update)
17-JUN-2002 (Rel. 41, Last sequence update)
18-JUN-2002 (Rel. 41, Last sequence update)
18-JUN-20
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                           SEQUENCE FROM N.A. STRAIN-BALB/c; TIS: MEDLINE-21442025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9D8D0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                            Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBCELLULAR
ALTERNATIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ittes requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELULIAR LOCATION: Type III membrane protein alternative PRODUCTS: 2 isoforms; 1 (shown here) produced by alternative splicing.
TISSUE SPECIFICITY: Detected in spleen, thymus, beart, and at lower levels in kidney and lung.
SIMILARITY: CONTAINS 1 THER-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:1343050;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIISLAVFYLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT
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117; Conser
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                              N.A. (ISOFORMS 1 AND 2).
TISSUE-B-cell lymphoma;
25; PubMed-11509692;
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CYTOPLASHIC (POTENTIAL).
TNER-CYS.
BY SIMILARITY.
   Qian F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 572; DB 1;
Pred. No. 8.7e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR SIGNAL-ANCHOR
                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                                                         Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
   Vora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175
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<u>.</u>
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                                                                                                                                                                                            Muridae; Murinae;
   Scott M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 185;
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RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,
RA Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl R., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sahai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Hordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-Oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Rah Kumpha-Locki A., Vonkida W., Mang K.H., Weltz C., Whittaker C., Wilming L.,
Rah Kumpha-Locki A., Vonkida W., Mang K.H., Weltz C., Whittaker C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cachero T.G., Hession Strauch K., Zafari M., Ambrose C.;
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yan M., Brady
Cancro M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wynshaw-Boris A., Yoshida K.,
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Small intestine; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;
"Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harless S.M., Lentz V.M., Sah A.P., Hilbert D.M., Hayes C.E., Cancro M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21475520; PubMed=11591325;
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FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLyS
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njamin C.D., Tschopp J., Browning
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EMBL; AF373847; AAK91827.1; -. EMBL; AK008142; BAB25490.1; -.

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EMBL; AK008142; BAB25490 MGD; MGI:1919299; Tnfrsf

Signal-anchor;

Transmembrane; Glycoprotein;

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"Cloning and characterization of the bovine Fas.";

"Cloning and characterization of the bovine Fas.";

DNA Cell Biol. 15:227-234(1996).

-I- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral reference in the antiqen-stimulated suicide of mature T-cells, (
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       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 6
receptor) (Apoptosis-mediating surface antigen FAS)
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                                                                ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                          SUBCELLÜLAR LOCATIÓN: Type I membrane protein. DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS. SIMILARITY: CONTAINS 3 TMFR-CYS REPEATS. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                   tolerance, in the antigen-stimulated suicide of both (By similarity).
                                                              SWISS-PROT entry is copyright. It is produced through a collai
een the Swiss Institute of Bioinformatics and the EMBL outsi
European Bioinformatics Institute. There are no restrictions
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Pfam; PF00531; death; 1.
SMART; SM00005; DEATH; 1
SMART; SM00208; TNFR; 3.
                                Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
Tumor necrosis factor receptor
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Q96RJ3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDEFKNTGSG-----LLGMANIDL-----EKSRTGD--EIILPRGLEYTVEECTCED
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P25445; IDDF.
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                                                                                          (Human)
                                                                                                                BAFFR
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                                                                                                          el. 41, Last sequence create)
el. 41, Last annotation update)
el. 41, Last annotation update)
factor receptor superfamily member 13C (B cell-
factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor)
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                                                                                                                                                                                                                                                                  STANDARD;
  (ISOFORMS 1 AND
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                                                                        Chordata;
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CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
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                                                      Craniata; Vertebrata;
Catarrhini; Hominidae
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No. 0.13;
2)
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                                                        Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 323;
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                                                                          Euteleostomi;
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Matches 48
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yan M., Brady J.R., Chan B., Lee W.P. Cancro M.P., Grewal I.S., Dixit V.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson J.S., Bixler S.A., Qian F., Y
Cachero T.G., Hession C., Schneider P
Strauch K., Zafari M., Benjamin C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF373846; AAK91826.1; Genew; HGNC:17755; TNFRSF13
                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of a novel receptor for B lymphocyte stimulator is mutated in a mouse strain with severe B cell deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21475520; PubMed=11591325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ambrose C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21442025;
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                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00652; PROSITE; PS50050;
                                                                                                                                                                                                                                                                                                                                                                                                MIM; 606269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *BAFF-R, a newly identified TNF receptor that specifically interacts
                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                Alternative
                                                                                                                                                                                                                                                                                                                                                             Receptor;
                       161
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T 178
                       T 161
                                                                     RTGDEIILPRGLEYTVEECTC-----
                                                                                                                  W---TCLGLSLIISLAVFVLMF----
                                                                                                                                         CVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGLL
                                                                                                                                                                 CSQNEYFDSLLHACIPCQL-----RCSSNTP--PLTCQRYCNASVTNSVKGTNAIL
                                              ---DKVII---LSPGISDATAPAWPPPGEDPGTTPP----GHSVPVPATELGSTELVTTK
                                                                                           FGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEP
                                                                                                                                                                                        1 Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293:2108-2111(2001)
                                                                                                                                                                                                                                                                                                                                                                                 PS00652;
                                                                                                                                                                                                                                                                                                                                                           Immune response;
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18
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24
143
184
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                                                                                                                                                                                        Conservative
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TNFR_NGFR_2; FALSE_NEG.
response; Signal-anchor; Transmembrane;
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143
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99
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                                                                                                                                                                                                                                                (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

TNER-CYS (PARTIAL).

BY SIMILARITY.

BY SIMILARITY.

P -> PA (IN ISOFORM 2).
                                                                                                                                                                                      Score 93; DB 1;
Pred. No. 0.088;
0; Mismatches
                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR
SIGNAL-ANCHOR
                                                                                                                                                                                                                                       F2BFB98099A27138 CRC64;
                                                                                                                  -LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS
                                                                    -EDCIKSKPKVDSDHCFPLPAMEEGATILVTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Vora K., Scott M.L.,
P., Sizing I.D., Mullen C.,
TSchopp J., Browning J.L.,
                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harless
                                                                                                                                                                                                              Length 184;
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                                                                                                                                         78
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PROM_MOUSE STAN 054990; 035408; 16-0CT-2001 (Rel. 4 16-0CT-2001 (R
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SIGNAL
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CARBOHYD
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miraglia S., Godfrey
Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
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Mammalia; Eutheria;
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                     CONFLICT
                                   CONFLICT
                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1100886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AF026269;
                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
   (Mouse)
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   Rodentia;
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N-LINKED (GLCNAC.
N-LINKED.
NISSING (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein tyrosine kinase 2 beta (EC 2.7.1.112)
2) (FADK 2) (Proline-rich tyrosine kinase 2) (beta) (CAK beta) (Calcium-dependent tyrosine)
adhesion focal tyrosine kinase).
PTK2B OR FAKZ OR PKZ OR RAFTK.
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                                                                                                                                                                                                                                                                                 Benzing T., Gerke P., Hoepker K., Hildebrandt F., "Nephrocystin interacts with Pyk2, p130(Cas), and phosphorylation of Pyk2.";
Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION OF TYR-402, AND INTERACTION WITH NEPHROCYSTIN MEDILINE-21396557; PubMed-11493697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                              Avraham S., London R., Fu Y., Ota S., Hiregowdara D. Pasztor L.M., White R.A., Groopman J.E., Avraham H.; "Identification and characterization of a novel relatyosine kinase (RAFTK) from megakaryocytes and braid. Biol. Chem. 270:27742-27751(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96070905; PubMed=7499242;
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induces the membrane-association of the kinase.
PTM: Phosphorylated on tyrosines in response to various stimuli that elevate the intracellular calcium concentration, as well a
                                              tyrosine phosphate.

SUBUNIT: Interacts with Crk-associated substrate (Cas), Nephrocystin and Grease regulator associated with PAK (Graf) SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocys
                                                                                                            downstream signals that regulate neuronal activity. Interacts the SH2 domain of GrD2. May phosphorylate the voltage-gated potassium channel protein Kvl.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase activity (By similarity).

CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                 FUNCTION: Involved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated receptors or neurotransmitters that increase calcium flux and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFVANQQTRTRIKGTQK------LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA
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Pred. No. 1
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D442F6372552B3C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Cell adhesion kinase kinase) (CADTK) (Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Focal adhesion kinase
                                                                                                                                                                                                                                                                                                                                                                                                                related adhesion brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                                                                                                  Kim E., Walz G.;
                                                                                                                                                                                                                                                                                                                  tensin
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                                              Nephrocystin
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Best Local S
Matches 29
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Pfam; PF03623; Focal_AT; 1.
Pfam; PF03623; Focal_AT; 1.
PRINTS; PR00109; TYRKINASE;
ProDom; PD000001; Euk_Pkinase; 1
SMART; SM00295; B41; 1.
SMART; SM00295; B41; 1.
                     TISSUB-Liver epithelium:
TISSUB-Liver epithelium:
MEDLINE-97094711; PubMed-8939945;
Yu H., Li X., Marchetto G.S., Dy R., Hunte
Wilm M., Anderegg R.J., Graves L.M., Earp
"Activation of a novel calcium-dependent;
Correlation with c-Jun N-terminal kinase;
Correlation with c-Jun N-terminal kinase;
                                                                                                                                                                                                                                                                                                                                      P70600; 063201; 068489;
15-JUL-1998 (Rel. 36, Casted)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein tyrosine kinase 2 beta (EC 2.7.1.112)
2) (FADK 2) (Proline-rich tyrosine kinase 2) beta) (CAK beta) (Calcium-dependent tyrosine left)
PTK2B OR FAK2 OR PYK2.
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protein kinase activation.";
J. Biol. Chem. 271:29993-29998(1996)
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                  672-687 AND 989-998
                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by PRC activation. Recruitment by were adhesions initiates Tyr-402 phosphorylation. In monocytes, adhesions initiates Tyr-402 phosphorylation. In monocytes, adherence to substrata is required for tyrosine phosphorylation and L-alpha and kinase activation. Anglotensin II, thapsigargin and L-alpha Lysophosphatidic acid (LPA) also induce autophosphorylation and increase kinase activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFKNTGSGLLGMANIDLEKSR------TGDEIILPRGLEYTVEECTCEDCIKSKPKV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50011; PROTEIN_KINASE_DOM; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR005189; Focal_AT IPR001245; Tyr_pkinase.
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Focal_AT.
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PHOSPHORYLATION (AUTO-) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
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                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                          AND
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                                                                                                                                                                                                          SEQUENCE
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                                                                                     Earp H
                                                                                       Hunter D.,
Earp H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding;
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                                         protein-tyrosine kinase.
but not mitogen-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ζ
                                                                                                                                                                                                          ဝှု
                                                                                                                                                                                                                                                                                                                                                               ) (Focal adhesion kinase (Cell adhesion kinase kinase) (CADTK).
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                                                                                                                Calvo
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                                                                                                                                                                                                                                                                         Euteleostomi;
; Murinae; Rat
                                                                                                             В.,
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                                                                                                                  Dawson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                         Rattus.
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SMART; SM00295; B41; 1.

SMART; SM00295; B41; 1.

PROSITE; PS00107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.

1. SUBUNIT: Isoform 1, but not isoform 2, interacts with Crk-associated substrate (Cas), Nephrocystin and GTPase regulator associated with FAK (Graf).

1. SUBCELULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin induces the membrane-association of the kinase (By similarity).

1. Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.

1. ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2/PRNK and 3/PYK2s; are produced by alternative splicing.

1. TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the brain (hippocampus, cerebral cortex and olfactory bulb) and poorly in the spleen and other tissues, whereas isoforms 2 and 3 are expressed in the spleen and brain (highest in cereballum).

1. PTM: Phosphorylated on tyrosines in response to various stimulication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adhesion kinase-related protein.";
J. Cell Sci. 111:1981-1991(1998).
-i- FUNCTION: Involved in calcium
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xiong W.-C., Macklem M., Parsons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98311659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.
"Cloning and characterization of cell adhesion kinase beta, a nov
protein tyrosine kinase of the focal adhesion kinase subfamily.";
J. Biol. Chem. 270:21206-21219(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-95403356; PubMed-7673154;
                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                    entities
                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Expression and characterization of splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                      InterPro;
                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                    by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                               by PKC activation. Recruitment by Nephrocystin to ceil matrix adhesions initiates Tyr-402 phosphorylation (By similarity). I monocytes, adherence to substrata is required for tyrosine phosphorylation and kinase activation. Angiotensin II, thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induautophosphorylation and increase kinase activity.

SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Involved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP + a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors or neurotransmitters that increase calcium flux and downstream signals that regulate neuronal activity. Interacts the SH2 domain of Grb2. May phosphorylate the voltage-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potassium channel protein Kvl.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase
                                                                                                                                                                                                                            U69109; AAC52895.1; -. D45854; BAA08290.1; -.
                                                                                                                                                                                          P00523; 2PTK.
                                                                                                                                                                                                          AF063890; AAC28340.1;
                                                                                                                                                                                                                                                                                    an
PS00107; PROTEIN_KINASE_ATP; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                    requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elevate the intracellular calcium concentration, as well as
                                                                                                                                                  IPR000719;
IPR005189;
                                                                                                              IPR001245; Tyr_pkinase
0069; pkinase; 1.
                                                                                                                                                                                                                                                                                  equires a license agreement (See http://www.isb-sib.ch/announce/
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A. (ISOFORMS 2 AND 3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9645946;
                                                                                                                                                  Euk_pkinase
Focal_AT.
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                                                                                                                                                                                                                                                                                                                                                                                           It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                    There are no restrictions ong as its content is in
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ALD DEFINITION OF THE PROPERTY OF THE PROPERTY
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FAK2_HUMAN
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CONFLICT
CONFLICT
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NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAK2_HUMAN STANDARD; PRT; 1009 AA. 0,014289; Q16709; Q13475; Q14290; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Protein tyrosine kinase 2 beta (EC 2.7.1.112) 2) (FADK 2) (Proline-rich tyrosine kinase 2) (beta) (CAK beta) (Calcium-dependent tyrosine kinase 2) (beta) (CAK beta) (Calcium-dependent tyrosine kinase 2)
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VARSPLIC
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MOD_RES
Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.; "Cloning and characterization of cell adhesion kinase beta, a novel protein-tyrosine kinase of the focal adhesion kinase subfamily."; J. Biol. Chem. 270:21206-21219(1995).
                                                                                                                                                                        MEDLINE-96435932; PubMed-8838818; Herzog H., Nicholl J., Hort Y.J., Herzog H., Nicholl J., Hort Y.J., "Molecular cloning and assignment adhesion kinase, to 8p11.2-p22 by Genomics 32:484-486(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adhesion focal tyrosine kinase). PTK2B OR FAK2 OR PYK2 OR RAFTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                     MEDLINE=95403356; F
                                                                                                                                                                                                                                                                                                                                                                                      Lev S., Moreno H., Martinez R., Canoll P.,
Plowman G.D., Rudy B., Schlessinger J.,
"Protein tyrosine kinase PYK2 involved in
of ion channel and MAP kinase functions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                          TISSUE-Hippocampus;
MEDLINE-96435932; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  Nature 376:737-745(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95379967; PubMed=7544443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ia; Eutheria;
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                                                                                                                                      FROM N.A. (ISOFORM
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(inase; Transferase;
                                                                                          PubMed=7673154;
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Primates;
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26.9%;
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
MISSING (IN ISOFORM 2).
NYFKRHSMR -> MGLIVLSSQ (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOCAL ADHESION TARGETING (FAT).
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ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canoll P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D435A475BCA49E9B CRC64;
                                                                                                                                                                                                      , Sutherland G.R. t of FAK2, a nove y nonisotopic in
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                                                                                                                                                                                                                                                                                                                                                                                                               Ca(2+)-induced regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peles
                                                                                                                                                                                                                            novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) (Focal adhesion kinase (Cell adhesion kinase kinase) (CADTK) (Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1009;
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;
                                                                                                                                                                                                      situ hybridization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Musacchio J.M.,
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EMBL;
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Benzing T., Gerke P., Hoepker K., Hildebrandt "Nephrocystin interacts with Pyk2, p130(Cas), phosphorylation of Pyk2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avraham
Pasztor
                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Menzel U., Schilhabel M.B., Submitted (OCT-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocytes. Activation by a two-stage process involving adherence subsequent intracellular signal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Monocytes;
MEDLINE=98211954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Passtor L.M., White R.A., Groopman J.E., Avraham H.; "Identification and characterization of a novel related tyrosine kinase (RAFTK) from megakaryocytes and brain."; J. Biol. Chem. 270:27742-27751(1995).
                                                                                                                               or send
                                                                                                                                                           entities
                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blechschmidt
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MEDLINE=96070905; PubMed=7499242;
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION OF TYR-402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nephrocystin and GTPase regulator associated with FAK (Graf).
SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin induces the membrane-association of the kinase.
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
TISSUE SPECIFICITY: Most abundant in the brain, with highest levels in amygdala and hippocampus. Low levels in kidney. Also expressed in spleen and lumnhorwer.
                                                                                                                                                                                                                                                                                                                                                               expressed in spleen and lymphocytes.

PTM: Phosphorylated on tyrosines in response to various stimul that elevate the intracellular calcium concentration, as well by PKC activation. Recruitment by Nephrocystin to cell matrix adhesions initiates Tyr-402 phosphorylation. In monocytes, adherence to substrata is required for tyrosine phosphorylatio and kinase activation. Angiotensin II, thapsigargin and L-alph lysophosphatidic acid (LPA) also induce autophosphorylation and increase kinase activity (By similarity). SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   downstream signals that regulate neuronal activity. Interacts the SH2 domain of Grb2. May phosphorylate the voltage-gated potassium channel protein Kv1.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase activity. ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine phosphate. SUBUNIT: Interacts with Crk-associated substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Involved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent
; U33284; AAC50203.1;
; L49207; AAB47217.1;
; D45853; BAA08289.1;
; U43522; AAC05330;1;
                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinfi
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an important signaling intermediate between neuropeptide activated receptors or neurotransmitters that increase calcium flux and the
                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                               a requires a license agreement (See http://www.isb-sib
an email to license@isb-sib.ch).
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                                                                                                                                                                                  is not removed.
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            von Buelow G.-U., Bram R.J.;
"NF-AT activation induced by a CAML-interacting necrosis factor receptor superfamily.";
Science 278:138-141(1997).
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                                                                                                                                                                                                                                                                              activator and CAML interactor)
TNFRSF13B OR TACI.
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Tumor necrosis factor receptor superfamily member 13B
                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
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G -> P (IN REF. 2).
F -> L (IN REF. 2).
R -> G (IN REF. 2).
R -> G (IN REF. 2).
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Nat. Immunol. 1:252-256(2000)
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Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinke
Migone T.S., Nardelli B., Wei P., Ruben S.M., Ull.
Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
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         Similarity
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         8.1%;
19.9%;
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 35;
                                                 TNER-CYS 2.
BY SIMILARITY
CHARLES (GLCNAC...
P-> L (IN REF. 2).
                   Score 78.5;
                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
TNFR-CYS 1.
          Pred.
                                                                                                                                                                        (POTENTIAL).
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                                                                                                                                                                                             EXTRACELLULAR
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                                        -> L (IN REF. 2)
411799F3DE17A5EB
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          No.
                                                                                                                                                                                                                 Transmembrane;
                      ВВ
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Dimke D., La
                                                                                                                                                                                 (POTENTIAL).
(TYPE III MEMBRANE
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 73;
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Ullrich S.J.,
                                           CRC64
                                                            .) (POTENTIAL)
                     Length 293;
 Indels
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                                                                                                                                                                                                                 Glycoprotein;
 57;
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Gaps
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                                                                                                                                                                 EMBL; U67575;
HSSP; Q54397;
TIGR; MJ1357;
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96337999; PubMed=8688087; Zhou L., Fleischmann R.D., Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Reich C.I., Cverheek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Keiley J.M., Peterson J.D., Sadow P.M., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                             TRANSMEM
                                                                                                                                                                                                                                             use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                        Pfam; PF02080; TrkA-C; Pfam; PF02254; TrkA-N;
                                                                                                                   InterPro; IPR001622; K+channel_pore
InterPro; IPR000309; TrkA_Kuptake.
InterPro; IPR003148; TrkA_N.
                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein
-!- SIMILARITY: STRONG, TO M.JANNASCHII MJ0138.1.
-!- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
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 SEQUENCE
                                                                        Hypothetical
                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                                          protein; Transmembrane; Transport;
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Query Match

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RESULT
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L., Barshi T., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Oxido T., Furuno M., Aono H., Baldarelili R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriyuez I., Sakamoto N.,
RA Mayashaw-Boris A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Nordone P., Soshida K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Nordone P., Soshida K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Nordone P., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Nordone P., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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T 15-JUN-2002 (Rel. 41, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last annotation update)
T 10-JUN-2002 (Rel. 41, Last annotation update)
T 10-JUN-2002 (Rel. 41, Last annotation update)
T 10-JUN-2002 (Rel. 41, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last sequence update
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MEDLINE=20341628; PubMed=10880535; Xia X.-Z., Treanor J., Senaldi G., Khare S.D., B Theill L.E., Colombero A., Solovyev I., Lee F., Miner K., Hawkins N., Guo J., Stolina M., Yu G.,
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MEDLINE-21177254;
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S.A., Grewal I.S.,
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                                                                                                                                                                                                             mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                             CDNA
Boone T., Kelley M.,
, McCabe S., Elliott R.,
, Wang J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSDHCF-PLPAMEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus.
                                                                                                                                                                                                                                                                                             1 K.-F.,
lming L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
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DISULFID
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                            Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meng S. Y., Boyle W.J., Hsu H.;
"TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
factor family member involved in B cell regulation.";
J. Exp. Med. 192:137-143(2000).
                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMIG with its C-terminus (By similarity).
-i- SUBCELULAR LOCATION: Type III membrane protein (Probable).
-i- SIMILARITY: CONTAINS 2 TNER-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                     143
                                            163
                                                                                           105
                                                                    92
                                                                                                                  54
                                                                                                                                          47
                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBUNIT: Bin
GFAGTAAPQPCMR - - ATV
                     CF----PLPAMEEGATI
                                           PRGSQANSPHAHRPVTEACDEVTASPQPVE---
                                                                                                                                         QGRYYDHLLGACVSCDSTCTQH---PQQCAHFCEKRPRSQANLQPELGRPQAGEVEVRSDN
                                                                                                                                                                QNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCN---ASVTN-----SVKGTN
                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:1889411; Tnfrsf13b.
[TE; PS00652; TNFR_NGFR_1;
                                                                    TGSGLLGMANIDLEKSRTGDEIIL-PRGLEYTVEECTCEDCI------KSKPKVDSDH
                                                                                           SGRHQGSEHGPGLRLSSDQLTLYCTLGVCLCAIFCCFLVALASFLRRR--GEPLPSQPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF257673; AAG000081.1; -. AK004668; BAB23457.1; -.
                                                                                                                                                                                       1 Similarity
43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                         THIRDING
                                                                                                                                                                                                                                      249
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                          150
                                                                                                                                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                                                                                                      response;
                                                                                                                                                                                                                                                 249
38
76
19
34
38
38
58
72
75
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149
                                                                                                               ----ILWTCLGLSLIISLAVFVL---MFLLRKISSEPLKDEFKN
                                                                                                                                                                                                   8.0%;
21.7%;
                                                                                                                                                                                                                                      ¥.
                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                       Signal-anchor;
                                                                                                                                                                                                                                                BY SIMILARITY
                                                                                                                                                                                                  Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC
TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                      CB2F2D61C2931D81 CRC64;
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                  (IN REF.
                                                                                                                                                                                                             BB
                                            -TCSFCFPERSSPTQESAPRSLGIH
                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Repeat
                                                                                                                                                                                                              <u>--</u>
                                                                                                                                                                                      70;
                                                                                                                                                                                                              Length 249
                                                                                                                                                                                       Indels
                                                                                                                                                                                       64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in no way
                                                                                                                                                                                      Gaps
                                                                                                                 91
                                                                                         162
                                                                                                                                         104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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RESULT
YCSB_SC
                                                                                     RA Wood V. Gwilliam R. Hayles J., Baker S., Basham D., Bowman S., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Ra Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Ra Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Handson G., Ra Hooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA McDonald S., McLean J., Wilter K., Green J., Squares R., Squares S., Stevens K., Sharp S., Stevens K., Starp S., Stevens K., Sharp S., Sharp S.,
                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCSB_SCHPO
074910;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Hypothetical WD-repeat protein C613.12c in
SPCC613.12C.
                                                                                                                                              PROSITE; PS00678, WD_REPBATS_1; 2.
PROSITE; PS50082; WD_REPBATS_2; 2.
PROSITE; PS50294; WD_REPBATS_REGION; 1.
Hypothetical protein; Repeat; WD repeat
REPEAT 297 336 WD 1.
REPEAT 486 525 WD 2.
                                                                                                                                                                                                                                                                                                                InterPro; IPR001680; WD40 Pfam; PF00400; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fundi; Ascomycota; Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHPO
                                                                                                                                                                                                                                                                                                                                                         EMBL; AL031644; CAA21064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                        ; PR00320; GPROTEI
SM00320; WD40; 4
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                            587
638
    Conservative
                                                                                   A
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                                                                                                                                                                                                                                                                                              GPROTEINBRPT
                                                                                 525
583
626
71536
                    7.8%;
22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomycetes;
Schizosaccharomycetaceae;
                                                                                   Ŧ
    20;
                    Score 75.5;
Pred. No. 1:
                                                                                                     WD 2.
                                                                                                                                                                  WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  otation update)
C613.12c in chromosome
                                                                                   6CD360D8748AAF98 CRC64;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ã
                                        DB 1;
                                        Length 638;
  indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    III.
  69;
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ourg S.L.,
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  Gaps
7;
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RESULT
SRK6_B
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     Pfam;
Pfam;
Pfam;
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentations are content to the content of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.; "Molecular cloning of a putative receptor protein kinase ge at the self-incompatibility locus of Brasslota Oleracea."; Proc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).
-!- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q09092;
                                                                                                                                                                                                       entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRK6_BRAOL
                                                         InterPro; IPR002290;
InterPro; IPR000858;
                                                                                             InterPro; IPR003609;
InterPro; IPR004040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. S6S6; TISSUE-Stigma;
MEDLINE-92020942; PubMed-1681543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica oleracea (Cauliflower).
                                                                                                                                   InterPro; IPR001480; B_lectin.
InterPro; IPR000719; Euk_pkina
                                                                                                                                                                         EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (S-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 YKKNKKLLPDYLKS
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                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein:
TISSUE SPECIFICITY: PREDOMINARTLY IN THE PISTIL AND ANTHER.
PISSUE SPECIFICITY: REPOMINARTLY IN THE PISTIL AND ANTHER.
POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN
B. CLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY
SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
GLYCOPROTEIN OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
A SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC DOMAIN.

CATALYTIC ACTIVITY: ATP + a protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FERTILIZATION), PROBABLY ACTING IN COMBINATION WITH S-LOCUS-SPECIFIC GLYCOPROTEINS. INTERACTION WITH A LIGAND IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR DOMAIN TRIGGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-----PNSRPYLSERVRKHTHL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEEC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIYDPFYRAELPCP------KPSLSISKHSIAKVPSNVNKR------LELQLLLTSGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLGLSLIISLAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKLKFGPVNSVQFNDAYSTHISPKLPGRAYEDC----QKFEIDNPSLSPVDKHGAIILRT
PF00069; pkinase; 1.
PF00954; S_locus_glycop; 1.
PF01453; Agglutinin; 1.
                                                                                                                                                                   M76647; AAA33000.1; ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase) (SRK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- DYCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                                                         STY_pkinase.
Ser_thr_pkin
                                                       Slocus_glycop.
                                                                                                                                 Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TCEDCIKSKPKVDSDHCFPLPAMEEGATILVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LSNSITGDDKPSLIHVDFTPEECFILQE
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                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a phosphoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene encoded
                                                                                                                                                                                                                                                                                                     a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosidae;
                                                                                                                                                                                                                                                                                                   outstation
                                                                                                                                                                                                                                             commercia
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ERBULLT
ID LET
ID LET
ID CR
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Matches 33
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P41771;
01-NOV-1995
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01-NOV-1995
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SMART;
SMART;
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                                                                                                                               Dean N.; "Cloning and DNA sequence of a Kluyveromyces lactis ERD1 homologue. Yeast 10:1117-1124(1994).
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PROSITE: PS00118; PROTEIN_KINASE_DOM; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                               MEDLINE=95084639; PubMed=7992512;
                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
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Eukaryota; Fungi; Ascomycota;
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                                                                            FUNCTION: REQUIRED FOR THE PRETICULUM PROTEINS, AFFECTS
                         GOLGI APPARATUS.
SUBCELLULAR LOCATION:
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SM00108; B_lectin; 1.
SM00473; PAN_AP; 1.
SM00221; STYKC; 1.
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32,
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17.6%; Pred. No. 23;
tive 30; Mismatches
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ATP (BY SIMILAR
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                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                      Pfam; Projice, Endoplasmic reticulum; Transmembrane; P
Endoplasmic reticulum; Transmembrane; P
POTENTIAL.
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162
                        129
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                                                   -FYIFAMILR--SSAMVARCFKR----ILWVADIEPKPYRNNYIIISDTLTSY------
                                                                            AVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTC
                                                                                                        SSLKLFKSISRVIIPWQLVC-----IILFQY---SFTNNV--SNKLLWFFLNVSPLLEL
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                       EDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK
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43; Conserv
-SKPLVD----
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Pred. No. 11
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Search completed: November 12, 2002, 16:58:58 Job time: 17.794 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
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4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organell:
9: sp_phage:*
10: sp_plant:*
11: sp_vius:*
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13: sp_verteb:*
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Gapop 10.0 , Gapext 0.5
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964
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sp_phage: *
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sp_vertebrate: *
sp_unclassified: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMD	
MARIES	

16	15	14	13	12	11	10	9	8	7	Ō	u	4	ω	2	1	Result No.
78	78.5	78.5	79.5	80	81	81	81.5	81.5	82	83.5	83.5	85.5	86.5	88.5	116.5	Score
8.1	8.1	8.1	8.2	8.3	8.4	8.4	8.5	8.5	8.5	8.7	8.7	8.9	9.0	9.2	12.1	Query Match 1
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Q8r2z1 mus musculu	Q9h677 homo sapien	Q8vfw0 mus musculu	Q26489 spodoptera	O81820 arabidopsis	001892 caenorhabdi	Q39191 arabidopsis	Q94711 paramecium	Q8vev6 mus musculu	097491 ovis aries	Q9str8 arabidopsis	Q8rwv7 arabidopsis	Q9y1x8 ephydatia f	Q8r056 mus musculu	Q97d61 clostridium	Q8r4w8 mus musculu	Description

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7.5	7.5	7.5	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.9	7.9	7.9	•	7.9					8.0	
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Q9zqr4 arabidopsis			Q9lmp0 arabidopsis	Q9zwd7 arabidopsis	Q8tmw0 methanosarc		Q40096 ipomoea tri	Q8t259 dictyosteli	Q97rg2 streptococc	Q91000 gallus gall	Q9rhu5 streptomyce	Q22378 caenorhabdi	Q9ykv7 human immun	Q9bi07 entamoeba h	Q8t206 dictyosteli	Q97e85 clostridium	Q8tlt4 dictyosteli	Q63661 rattus norv	042637 neurospora	045251 caenorhabdi	Q9fje3 arabidopsis	C	Q9x0n0 thermotoga		004623 arabidopsis			Q91mn6 arabidopsis

ALIGNMENTS

### BRAINS PRELIMINARY; PRT; 175 AA. ##################################	RESULT	Oy dd	Qу	Qy	Que Bes Mat	SQ	DR i	æ ;			7 7 7	Z				DE	ď			Ħ	Q8R4W8
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QROSS
ID QROSS
AC QROSC
DT 01---
DT 01---
DT 01---
DT 01---
DE Hypo
OS Muss
OC Eukk
OC Eukk
OC NCDI
RN (1)
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SEQUE
RA SECUE
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Best L
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Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Noelling J., Breton G., Omelchenko M.V., Makarova Gibson R., Lee H.M., Dubois J., Olu D., Hitti J., Tatusov R.L., Sabathe F., Doucette-Stamm L., Souca Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the spacterium Clostridium acetobutylicum."; J. Bacteriol. 183.4823-4838(2001).

EMBL; AE007858; AAK81542.1; EMBL; AE007858; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid ABC transporter, CAC3619.
                                            Strausberg R.;
Submitted (APR-2002) to the
EMBL; BC028286; AAH28286.1;
Hypothetical protein.
SEQUENCE 842 AA; 94478 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q97D61;
01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2001 (TrEMBLrel. 18,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q97D61
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium acetobutylicum
                                                                                                                                                                     TISSUE-EYE;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                 Hypothetical 94.5 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8R056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21359325; PubMed=11466286;
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  Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLLHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLIISLAVEV--LMFLLRKISSEPLKDEF----KNTGS-----GLLGMANIDLEKSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSLNKVIPVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT
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217 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
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Last annotation update)
                                                                                                                       EMBL/GenBank/DDBJ
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Pred.
                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                 734C10D715E5BC92
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86.5;
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DB
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                                                                                                                       databases
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Length 842;
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                                                                  ProDom: PD000001; Euk_Pkinase;
SMART: SM002261; FU; 6.
SMART: SM00220; S.TKC; 1.
SMART: SM00219; TYTKC; 1.
                                                                                                                                                                                                                                    EMBL; AB006570; BAA81724.2;
HSSP; P08631; 1AD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Porifera
Haplosclerida; Spongillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                  PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                             Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain;
                                                                                                                                                                                                                                                             parazoan-eumetazoan split.
Gene 280:195-201(2001)
                                                                                                                                                                                                                                                                                    domain shufflings in the early
                                                                                                                                                                                                                                                                                                           MEDLINE=21601119; PubMed=11738833;
Suga H., Katoh K., Miyata T.;
                                                                                                                                                                                                                                                                                                                                                                   "Extensive gene duplication in the early eventhe parazoan emmetazoan split demonstrated tyrosine kinases from sponge and hydra.";
                                                                                                                                                                                                                                                                                                                                                                                                        Miyata
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                       PROSITE;
                                                                                                                   PRINTS; PRO0109; TYRKINASE
                                                                                                                                                                  InterPro; IPR001368;
InterPro; IPR001245;
                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                    InterPro; IPR000719;
InterPro; IPR002174;
                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                 "Sponge homologs of vertebrate
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=31330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999
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                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL--
                                                                                                                                                                                                                                                                                                                                                         Evol. 48:646-653(1999).
                       PS00652;
                                                                                                                                                                                          IPR002290;
                                                                                                                                                                                                                            IPR000494;
 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
3
                     TNFR_NGFR_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porifera;
                                                                                                                                                                  Tyr_pkinase.
                                                                                                                                                                             Ser_thr_pkinase
TNFR_c6.
                                                                                                                                                                                                    Furin-like
                                                                                                                                                                                                                             EGFR_L_domain
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 128169
                                                                                                                                                                                                               Euk_pkinase.
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20,
21,
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Last annotation update)
M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydatia.
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                                                                                                                                                                                                                                                                                     protein tyrosine kinases and frequent evolution of animals before the
                       UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
009E4AC9BC12DF60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    ono
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                                                                                                                                                                                                                                                                                                                                                                                             evolution of animals before
                                                                                                                                                                                                                                                                                                                                                                                γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ceractinomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                    Iwabe
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                                                                                                                                                                                                                                                                                                                                                                                G
                                                                                                                                                                                                                                                                                                                                                                                proteins
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RESULT
Q9STR8
ID Q8
AC Q9
DT 00
DT 00
DT 01
DE HH
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Hypothetical 103.6 kDa protein.
AT3648195.
Q9STR8
Q9STR8;
Q1-MAY-2000 (
01-MAY-2000 (
01-DEC-2001 (
01-DEC-2001 (
Hypothetical
T24C20_80.
                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Reyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki Davis R.W., Ecker J.R., Theologis A.;
"Arabidopsis Full Length CDNA Clones.";
"Arabidopsis Full Length CDNA Clones.";
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AY091078; AAM13898.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8RWV7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8RWV7
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein SEQUENCE 938 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              821
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                                                                                                                                                  114 DGGATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQRYCNASYTNSVKGTNAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRP------PKLPPDATRLITPETALEQGQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILPRGLEYTVEECTCEDCIKSKPKVDSDH----CFPLPAMEEGATI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTCLGLSLIISLA---VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEI
                                                                                                                                                                          EEGATI
                                                                                                                                                                                                                                                                                     QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIVFGSIVVIFLATSIVLILFIVYRRYEHKVFKNRTQSTA---MCYSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCVSGCSNDTEYQDAALN-CLPCAAGCIGCSGPSISQCLTCA--SGSCTTTDVQSSGGII 771
                                                                                                                                                                                                     SLVKLSSLDM--SRLGD---
                                                                                                                                                                                                                                GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLPAM
                                                                                                                                                                                                                                                            ERYCSA---NSALGTPSM--
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                                                                                                                                                                                                                                                                                                              1 Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
             (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
1 223.5 kDa protein.
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                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  103602 MW;
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22.3%;
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                                                                                                                                                                                                       -RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--M
                                                                                                                                                                                                                                                                                                                            Score 83.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 85.5; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                    3E78395D65D75C95 CRC64;
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                                                                                1998
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                                                                                                                                                                                                                                                                                                               28;
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                                                                                                                                                                                                                                                                                                                                         938
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Best Local S
Matches 37
Pfam; PF00531; death; 1.

Pfam; PF00020; TNFR_C6; 3.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

SMO208; TNFR; 3.

PROSITE; PS00652; TNFR_NGFR_1; 1.

PROSITE; PS00652; TNFR_NGFR_2; 2.

SEQUENCE 327 AA; 36928 MW; 5CFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999
01-MAY-1999
01-JUN-2001
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
EMBL; ALO96856; CAB51067.1; .
InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choisne N., Robert C., Brottier P., Wincker P., Cattoli Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K., Mayer K.F.X., Quetler F., Salanoubat M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Choisne N., Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   097491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 1998 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00787; PX; 1
SMART; SM00312; PX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                  Submitted (MAR-1998) to the EMBL; AB011671; BAA37093.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Caprinae; Ovis
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
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                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                Takagi M., Takahashi H., Kabeya
"Cloning of sheep fas antigen."
                                                                                                                                                                                                                                                                                                                                                               TISSUE=LYMPHOCYTE;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150
                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                   InterPro; IPR000488; Death
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nes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGGATI 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLVKLSSLDM--SRLGD-----RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--M 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLPAM
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                                                                                                                                                                                                                                             P25445; 1DDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001683;
                                                                                                                                                                                           IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 10, (TrEMBLrel. 10, (TrEMBLrel. 17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223513 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 83.5; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
  1,
2,
5CFEE844B2BE387A CRC64;
                                                                                                                                                                                                                                                                                                                                     н.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                        Ohashi K.,
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                   01-FEB-1997
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51C surface
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01factory receptor MOR202-36.
Mus musculus (Mouse)
                                                                                                               Q94711
Q94711;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
Paramecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                           CSQNEYFDSLLHACIP-CQLRCSSNT-----PPLTCQRYCNASVTNSVKGTNAILWT
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                                                                                                                                                                                                                                                     CDGILTLLVILNTYLLIFIAILRMRSAEAQRKAFSTCASHLI
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                                                                                                                                                                                                                                                                                                                                               CYMCGILQSSIHVALAFCLSFCNSNVINHFFCDIPPL-LDISCSDTYTNEI--TVLILGT
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tetraurelia
                                     (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
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0:0-0(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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Last sequence update)
Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 81.5;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Best Local
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                        Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00179; EGF_CA; 1.

SMART; SM00019; EGF_Like; 1.

SMART; SM00001; EGF_Like; 1.

PROSITE; PS00101; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_T; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-92106337; PubMed=1762150;

Nielsen E., You Y., Forney J.;

"Cysteine residue periodicity is a conserved structural feature
                                                                                                                                                                                                                                                                                                                                                                              eurosids II; Brassicales;
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q39191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variable surface proteins from Paramecium tetraurelia.";
J. Mol. Biol. 222:835-841(1991).
EMBL; M65164; AAA61740.1; ..
                                                                                                                                        InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                 InterPro; IPR000152;
InterPro; IPR000561;
InterPro; IPR001881;
                                                                                                                                                                                                                           EMBL; L04999; AAA32844.1;
                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 89:10989-10992(1992).
                                                                                                                                                                                                                                                                                "An Arabidopsis serine threonine kinase homologue with selected in yeast for its specificity for a thylakoid r
                                                                                                                                                                                                                                                                                                              Smith
                                                                                                                                                                                                                                                                                                                          MEDLINE=93066369; PubMed=1438303;
                                                                                                                                                                                                                                                                                                                                         STRAIN-COLUMBIA
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            039191;
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               ATP-binding;
                                                                                                                                                                                                                                                                    protein."
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nes 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTVEECTC----EDCIKSKPKVDSDHCFPLPAMEEGATI-----LVTTKTN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTVELCEAYKPSSNCV---PNGTKKGCMELAAKCESRTIKEQCDVAGTKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDL----EKSRTGDEIILPRGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSCYQKQ------CSAASQDNTTHAQCQEYLPACTLSNTKKG------CIDLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA-SVTNSVKGTNAILWTCLGLSL
                                                                                                                                                                                                                                                                                                           T.A., Kohorn B.D.;
 Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
               Calcium-binding; EGF-like domain;
                                                                                                                                                                                 EGF-like.
EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.5%;
25.1%;
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                                                                                                                                                                                                                                                                                                                                                                                              Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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Last sequence update)
Last annotation update)
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595
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Transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
             Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2233;
                                                                                                                                                                                                                                          PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64
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                                                                                                                                                                                                                                                                                              EGF repeat
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                                                                                                                                                                                                                                                                                                                                                                                                              Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local
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                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               001892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. R08F11.7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R08F11.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997
                                                                                                                                                                                                                Submitted (JUN-1999) to the EMBL; AF003385; AAB54249.1; HSSP; P05164; 1CXP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                  Waterston
                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                   investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 TMSCKRKEFAWTTILLVTTIGF-LVILLGVACIQQRMKHLKDTKLREQFFEQNGGGMLTQ 245
                                                                                       184
304
                      124
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                                                                                                                                                                                                                                                                                               sequence of C. elegans cosmid RO8F11."; itted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GMANID------LEKSRTG--DEIILPRGLEYTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRCNEGFDGNPYLSAGCQDVNECTISSTIHRHNCSDPKTCRNKVGGFYCKCQSGYRLDTT 186
                                                                                                            PCQLRCSSNTPPLTCQ-----RYCN----ASVTNSVKGTNAILWTCL---GLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLSGPSNVDVKIFTEDGMKKATNGYAESRILGQGGQGTV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNSVK-----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSQNEYFDSLLHACIPCQ--LRCSSN-----TPPLTCQR-----YCNA-----SV
SSLNCTSC--SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ
                      EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA-----TE
                                                                IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV
                                                                                       PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA
                                                                                                                                                                                 PF03098;
NCE 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                    IPR002007; Anim_peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 04, (TrEMBLrel. 04, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                    Conservative
                                                                                                                                                                                 An_peroxidase;
AA; 83992 MW;
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                                                                                                                                              8.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81;
Pred. No.
                                                                                                                                               Score 81; DB Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7B58FC1A656E0641 CRC64;
                                                                                                                                                                                 4E3373FDA4EC67C7 CRC64,
                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            773
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                                                                                                                                                         DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                    91;
                                                                                                                                                        Length 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 595;
                                                                                                                                    Indels
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                                                                                                                                    28;
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PRODOM; PD000001; Euk_pkinase; 1.

R SMART; SM000179; EGF_CA; 1.

R SMART; SM000179; EGF_CA; 1.

R PROSITE; PS000101; ASX_HYDROXYL; UNKNOWN_1.

R PROSITE; PS01186; EGF_2; UNKNOWN_1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01018; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_DS; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                    Matches
                                                                                                                                                                                       Query Match
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Wall-associated kinase 1 (Putative wall-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL; AJ003696; CAA08794.1; -. EMBL; AJ00369917; AAK64021.1; -. InterPro; IPR000152; Asx.hydroxyl. InterPro; IPR000561; EGF-like. InterPro; IPR000561; EGF-like. InterPro; IPR0007619; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada K., Liu S.X., Sakano H., Pham P.K., Bahh J., Chung M.K., Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawal J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palim C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       He Z.H., Cheseman I., He D., Kohorn B.D.;
He Z.H. Cheseman I., He D., Kohorn B.D.;
"A cluster of five cell wall associated receptor kinase genes, Wak1-5, are expressed in specific organs of Arabidopsis.";
plant Mol. Biol. 39:1189-1196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            081820;
01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002290; Ser_thr_pkinase
InterPro; IPR004040; STY_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sakurai T., Satou M., Seki M., Shinn P., Southwick i Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene F16F4.6 (GI:8920634)."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99308512; pubMed-10380805; He Z.H., Cheeseman I., He D., Kohorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAK1 OR F16F4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
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324
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                                                                                                            CSQNEYFDSLLHACIPCQ--LRCSSN-----TPPLTCQR----YCNA-----SV 45
TMSCKRKEFAWTTILLVTTIGF-LVILLGVACIQQRMKHLKDTKLREQFFEQNGGGMLTQ
                                   TNSVK-----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
                                                                         CRCNEGFDGNPYLSAGCQDVNECTTSSTIHRHNCSDPKTCRNKVGGFYCKCQSGYRLDTT
                                                                                                                                                    Similarity
39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                     8.3%;
                                                                                                                                                27; Mismatches
                                                                                                                                                                       Pred.
                                                                                                                                                                                       Score 80;
                                                                                                                                                                       No.
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edons; core eudicots; Rosid
                                                                                                                                                                                          DB
                                                                                                                                                                                          10;
                                                                                                                                                    49;
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                                                                                                                                                                                          Length 735;
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                                                                                                                                                                                                                                                                       Kinase;
                                                                                                                                                  Gaps
                                     97
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-GMANID--

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RESCAPE DE 
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Best Local
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Pfam; PF00082; Peptidase_S8; 1.

PRINTS; PR00723; SUBTILISIN.

ProDom; PD000717; P_domain; 1.

SMART; SM00261; FU; 10.

PROSITE; PS00136; SUBTILASE_ASP; 1

PROSITE; PS00138; SUBTILASE_SER; 1

PROSITE; PS00138; SUBTILASE_SER; 1
                                                                                                                                                                                                       Q8VFW0;
Q8VFW0;
01-MAR-2002
01-MAR-2002
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Spodoptera frugiperda (Fall armyworm).

Bukaryota; Metazoa; Arthropoda; Trachbata; Hexapoda; Insect

Bukaryota; Metazoa; Arthropoda; Trachbata; Hexapoda; Insect

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

Pterygota; Neoptera; Ambhipyrinae; Spodoptera.
                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01factory receptor MOR202-16.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR000209; Peptidase_S8
InterPro; IPR002884; P_domain.
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases EMBL; Z68888; CAA93116.1; -.
HSSP: Q99405; IMPT.
     SEQUENCE
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema '
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Si
Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human CDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AKO26184; BAB15387.1;

SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank EMBL; AY073405; AAL61,068.1; ... Interpro; IPR000275; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GPCRRHODOPSN. PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                 CDNA: FLJ22531 fis, clone HRC12890.
Homo sapiens (Human).
Eukarrotts. wet--
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"The olfactory receptor gene
Nat. Neurosci. 0:0-0(2002).
[2]
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
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                        -EGATILVTTKTN
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Shibahara T.,
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Domain

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22-NOV-2001. WO200187979-A2

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21	21	21	23	22	22	22	22	22	22	23	23	. 20	23	23	22	21	22	21	22	22	21	21	21	21	6	16	22	22	21	21	22	22	23	20
AAG20000	AAG57044	AAG57045	ABG40174	AAM70525	ABB22692	ABB37396	ABB61371	ABB60972	AAU43223	ABP26712	ABP29975	AAY00870	AAU76341	AAU76340	AAB68985	AAG39947	ABB60009	AAG31130	ABB67383	ABB65832	AAG39948	AAG39949	AAG31131	AAG31132	AAP50343	AAR71259	AAU36711	AAU33894	AAG21218	AAG21219	ABB62925	ABG29063	ABP43259	AAY00040
Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human peptide enco	Human bone marrow	Protein #4691 enco		Drosophila melanog	Drosophila melanog	-		reptococcus	S. tuberosum isoam	Yeast D-arabinono-	Yeast D-arabinono-	æ	CO.	∍	SO.		Drosophila melanog		 Arabidopsis thalia 		٠. د	coded by clo			Ω			Drosophila melanog	n diagn	E faecalis EF017 p	Enterococcus faeca

ALIGNMENTS

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RESULT 1
ANALISA84
ID ANELISA84
AC AAEI
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AC AAEI
XX 12-W
XX 12-W
XX 12-W
XX Cytt
KW Cytt
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FFT Reg:
FFT Comark
FFT Domark
XX W021
PN W021
                                                                                                                                                                                          Key
Region
                                                                                                                                                                                                                                                                                                                                               Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                           Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human B-cell maturation (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE15484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE15484 standard; Protein; 181 AA.
                                                                                                                                                                                                                                                       HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                               /note= "Cysteine-rich consensus region; This is region is specifically claimed as SEQ ID NO: 7 in claim 1 of the specification" 52...72
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RESULT 2
AABO8843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                     BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                          кеу
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27-JUN-2000; 2000US-214591P-
14-MAY-2001; 2001US-0214591
31-AUG-2000
                                                                            Domain
                                                                                                                         Homo sapiens
                                                                                                                                                                                                                         Amino acid
                                                                                                                                                                                                                                                                                                                   AAB08843 standard; peptide; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 10A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-2001;
                             WO200050633-A1
                                                                                                                                                                                                                                                                                                                                                                                                   102 EKSRTGD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCMA protein
                                                                                                                                                                                                                       sequence of human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                      (first entry)
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                                                                          Location/Qualifiers 57..77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94pp; English.
                                                           "putative transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method
                                                                                                                                                                             systemic lupus crythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                       Homo
                                                                                                                                               graft
                                                                                                                                                                                                                                                       transmembrane activator and CAML-interactor; tumour necrosis factor; ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
                                                                                                                                                                                                                                                                                                                                A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                  20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY94001 standard; Protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 32; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-2000; 2000WO-US04925
                                 WO200040716-A2
                                                                                                                                                                                                                                                                                            Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                                                         renal artery stenosis;
                                                                                                                         immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic insulin dependent diabetes mellitus; Crohn's disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 EKSRTGD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dentifying
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                                                                     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that modulate NF-kB expression and thus for drug
                                                                                                           occlusion; cholesterol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                                                                                                           renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                           septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                             tor; TNF;
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Marsters

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Pitti RM;

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RESULT 4

ARABOS 14

ARABOS 27

AC AAEC

XX AAEC

XX AAEC

XX AAEC

XX Huma

DE Huma

XX Huma

XX Huma

XX PSO

XX PSO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell CC protein) receptor contain a cysteine rich domain, and are used for CC inhibiting zenf4 activity. Ztnf4 is a TNF ligand. They may also be used CC inhibiting zenf4 activity. Ztnf4 is a TNF ligand. They may also be used CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated CC with activated or resting B lymphocytes, effector T-cells, or with activity and contains a sacciated with an CC antibody production. The antibody production is associated with an CC antibody production. The antibody production is associated with an CC arthau for the contains and rheumatoid arthritis. The ztnf4 activity CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with CC asthma, bronchitis, emphysema, end stage renal failure, CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with CC asthma, bronchitis, vasculitis, nephritis, pyelonephritis, renal CC emplasms, multiple myelomas, lymphomas, light chain neuropathy. CC amyloidosis, moderating immune response, immunosuppression, graft CC election, graft versus host disease, inflammation, insulin dependent CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE09241 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JAN-2000;
28-NOV-2000; 2000WO-US32378
                                                 23-AUG-2001
                                                                                              WO200160397-A1
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                    autoimune disease;
                                                                                                                                                                                                                                         Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
                                                                                                                                                                                                                                                                                                                   Human BCMA protein
                                                                                                                                                                                                                                                                                                                                                                     19-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stenosis, or occlusion,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 EKSRTGD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EKSRTGD 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents a human BCMA protein, a B cell protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to transmembrane activator and CAML-interactor (TACI) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 152; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US00396
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                                                                                                                                                                                                                    rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholesterol or renal emboli.
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Pred. No.
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5.7;
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RESULT
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Best Local :
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                     06-OCT-1999;
11-FEB-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, ARIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthitis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity, for treating autoimmune disorders and cancer, comparencesing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                  systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-ceil lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                       gene therapy, cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human B cell maturation protein (BCMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE00506 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 2; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yan
                                                                                                                   05-OCT-2000;
                                                                                                                                                                     12-APR-2001
                                                                                                                                                                                                                    WO200124811-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psoriasis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 EKSRTGD 111
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DB; AAD15902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
                                                                                                                                                                                                                                                                                                             necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0
                     99US-0157933.
2000US-0181807.
2000US-0215688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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2000US-0226986
                                                                                                                      2000WO-US27579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lupus erythematosus. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dodge KH,
                                                                                                                                                                                                                                                                                                                factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 184
                                                                                                                                                                                                                                                                                                                BCMA; B cell maturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grewal I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kim KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB:
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Gaps

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Length 184; Indels

protein

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AAC AAB6

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AC AAB6

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DE Huma

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Huma

KW Lam

KW B-cg

KW Orgu

KW Orgu

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KW Orgu

KW U-chan

KW Orgu

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, lumunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hyperte renal disorder; immunosuppressive disorder; HIV infection; renal disorder; immunosuppressive disorder; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and 115 cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoms as a human line acceleration such as cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation inducing Ligand Receptor (ABDILE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 3A; 85pp;
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(APOT-)
                                                                                       22-FEB-2001
                                                                                                                                                 WO200112812-A2
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                             B-cell carcinoma; leukaemia; rapidly progressive
                                                                                                                                                                                                                                                                                                                          organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human BAFF receptor (BAFF-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-2001
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                             16-AUG-2000;
                                                                                                                                                                                                                                                                      Tympnoma;
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7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APOTECH R & D
                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
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                             2000WO-US22507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                   therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is human APRIL-R also referred as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ambrose C,
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                                                                                                                                                                                                                                                                                                glomerulonephritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension;
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AAY71979 standard; Protein; 184 AA

RESULT 7

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EKSRTGD 111

1 EKSRTGD 7

Matches Best

Local

Similarity 7; Conserv

Conservative

0;

Mismatches

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Gaps

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thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myssthenia gravis; chromosome 16: post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation

Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;

Human B cell maturation factor (BCMA) protein.

28-MAR-2001

(first entry)

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the TNF (tumour necrosis factor) family, acting as an immunoregulatory cagent, and also plays a role in the development of hypertension and crelated disorders. BAFF-R, fusion proteins contending it, and BAFF-R-C specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. B-cell lymphoproliferative conditions are the stream of the 
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1999;
11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                       progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                             Sequence
                                                                                                                                                         present sequence represents human BAFF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                184 AA;
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20000S-0181684.
20000S-0183536.
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100.0%;
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   Score 36;
Pred. No.
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DB 5.7;
                                 22;
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                                 Length 184;
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Homo sapiens

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RESULT 8
ABB81487
ID ABB8
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AC ABB8
AC ABB8
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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to Tumour necrosis factor (TNF) and Apol-related Leucovyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid autoitits associated autoimmune disorders like rheumatoid.
                                                                                                                                                                                                                                                                                                                                                                                                 spleen and lymph nodes but not by brain, muscle, heart, lung, k. pancreas, testis and placenta. BCMA mRNA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in diagnostic assays.

The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravus, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 37; Page 104-105; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -
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01-MAY-2000;
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                Human BCMA receptor related protein SEQ ID NO:7
                                                  02-SEP-2002 (first entry)
                                                                                                                      ABB81487 standard; Protein; 184
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                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                           1 EKSRTGD 7
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                                                                                                                                                                                                                                                                            Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                184 AA;
                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                              0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                          activities, and can be used in gene therapy. (1) can be used for chihibiting, in a mammal, the activity of a ligand that binds Ztufr12 (e.g. ZTNF4), for treating disorders and diseases associated with B CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for cinhibiting the proliferation of tumour cells. (1) is useful for treating CC autoimmune disorders such as systemic lupus erythematosus, myasthenia CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid CC leukaemia, nephritis, and pyelonephritis, and for treating renal CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or CC amyloidosis, hypertension, large vessel disease, graft-versus host CC disease, graft rejection and Crohn's disease. (1) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody
                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated human tumor necrosis factor receptor polypeptide, t 2tnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2000; 2000US-246449P
20-DEC-2000; 2000US-257131P
28-JUN-2001; 2001US-301715P
29-AUG-2001; 2001US-315565P
                                                                                                                                                                                                                                                                                                                                 production and cytokine production, and for modulating T and B communication. The present sequence represents a protein which given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     designated Ztnfr12 (I). (I) has cytostatut, ammunity antidiabetic, dermatological, antiinflammatory, neuroprotective, antidiabetic, antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive antirheumatic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, antirheumatic, help antirheumatic, antiarthritic, antiarthritic, antirheumatic, help antirheumatic, antiarthritic, antiarthritic, antirheumatic, help antirheumatic, antiarthritic, antiarthritic, antiarthritic, antiarthritic, antirheumatic, help antirheumatic, antiarthritic, antiart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                                                                                                                                                      Sequence
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RESULT 9 AAY00041

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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                    Enterococcus
                                        Enterococcus; vaccine;
                                                                E faecalis
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccines for preventing, treating c a member of the Enterococcus genus faecalis
 New isolated products for
                             WPI; 1999-070095/06
N-PSDB; AAX20030.
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                                                          Choi GH,
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Enterococcus faecalis polynucleotides the detection of Enterococcus and for
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                                                                                                                                                                                                                             faecalis; infection; vaccine; immune response; diagnosis;
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97US-0044031.
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                                                          Hromocky)
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                                                           Kunsch
                                                           CA.
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                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus; vaccine; gastrointestinal disease; diagnosis; antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EKSRTGD 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKSRSGD 432
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6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN98015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s and polypeptides from Enterococcus faecalis, useful for preventing, treating or attenuating an infection of the Enterococcus genus in an animal, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bailey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 AA;
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.78;
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1.2e+02;
0;
DB 23;
1,2e+02;
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                                     542;
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Query Match
Best Local :
                                                                                                                                                                             for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodwersity
                                                                                               and to produce other types of data and products dependent on D amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (III) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifier are also used in diagnostics as expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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23-AUG-2000;
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DB; AAS93250.
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upplement; medical imaging; diagnostic; genetic or

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 59422; 103pp;
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                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLG016-ABL30511), expressed DNA sequences (ABLG016-ABL30511), expressed DNA sequences (ABLG016-ABL30511).
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                                                                                                                                                                Sequence
                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 15567; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                    New isolated nucleic a
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N-PSDB; ABL07028.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
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           17-OCT-2000
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11-JUL-2000;
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6; Conser
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2000US-0614150.
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Pred. No. 2.4e
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and cell-cell
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23-MAR 1999
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26-MAR 1999
06-APR 1999
06-APR 1999
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Arabidopsis thaliana protein fragment SEQ Ħ ö 23696

Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; sequence

Arabidopsis thaliana

2000EP-0301439

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Search completed: November 12, 2002, 16:58:32 Job time: 3.67382 secs
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Patent No.
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                                                                                                                  APPLICANT: Martin, Catherine R
APPLICANT: Plant Bloscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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G11 H. Choi
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                           CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
                                                                                                                                                                                                                           APPLICANT: Edwards,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
              PRIOR APPLICATION NUMBER: GB 9716185.5 PRIOR FILING DATE: 1997-07-31
                                                PRIOR FILING DATE: 1998-07-30
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION INFORMATION
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                   426 EKSRSGD 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino a
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.5
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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5. 6448043
SEQ
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6; Conserv
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                                                                                                                                                                                       Smith, Alison M
Bustos Guillen, Regla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Human Cenome Sciences,
9410 Key West Avenue
ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                         Elizabeth A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.9%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB Pred. No. 30; 1; Mismatches
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144 KNRTGD 149

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; TYPE: PRT ; ORGANISM: Solanum tuberosum US-09-463-238-6
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US-08-424-641B-11
                                                                                         US-08-424-641B-11
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Best Local Similarity /1...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                Matches
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenbergh
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Resistance
                                                                                                                                                                            TELEFAX: (517) 347-410
TELEX: NO. 5824523e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Tan C. McLeod
REGISTRATION NUMBER: 20,931
                                                                                                        TOPOLOGY: Linear MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                         TELEPHONE: (517) 347-4100
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                              Local Similarity
les 5; Conserv
                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/366,480 FILING DATE: December 30, 1994
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/424,641B FILING DATE: April 19, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Okemos
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                                                                                                                                                                LENGTH:
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   2 KSRTGD 7
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                                                                                                                                                   Amino Acid
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                                                                                                                                                              288 Amino Acids
                                                                                                                                                                                                                         (517) 347-4103
                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ian C.
                                                                                                                                                                                                                                                                                                                                            December 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette,
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                                                                                                                                   Single
                                              77.8%;
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.25 inch, 360 Kb
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Pred. No. 1.1e+02;
Pred. No. 1.1e+02;
                                            Score 28; DB 2;
Pred. No. 1.2e+02;
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 766;
                                                           Length 288;
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                                Gaps
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RESULT 5 US-08-820-980-11

Sequence

Application US/08820980

Patent No.

GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: ACER
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOIDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
MEDIUM TYPE: storage
                                                                                          APPLICANT: Sylvain Moineau, Shirley A. APPLICANT: Walker, Ebenezer R. Vedamut APPLICANT: and Peter A. Vandenser A. Peter A. Vandenser A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,
FILING DATE: April 19, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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NAME: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 KNRTGD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/820,980 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 20,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KSRTGD 7
                                                                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sylvain Moineau, Shirley A. Walker, Ebenezer R. Vedamut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Peter A. Vandenbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Resistance
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                                                                  Isolated DNA Encoding
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                                   Enzyme For Phage
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Pred. No. 1.26
1; Mismatches
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                                                                                                                                         Vedamuthu,
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US-08-826-439-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 634258
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 553,
                EARLIER APPLICATION NUMBER: 60/051, 929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052, 803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052, 732
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FLING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/227,357
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: 123 FILE REFERENCE: PZ010P1
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TELEX: NO. 5972673e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    EARLIER APPLICATION NUMBER: 60/051,925 EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fischer et al.
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MEDIUM TYPE: Diskette
MEDIUM TYPE: storage
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,
FILING DATE: April 19, 1995
CLASSIFICATION: 530
CLASSIFICATION: 530
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NAME: Ian C. McLeod
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STRANDEDNESS: Sir
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TELEFAX: (517) 347-4103
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REFERENCE/DOCKET NUMBER: Quest 4.1-155
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NUMBER: 60/051,931
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Pred. No. 1.2e+02;
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US-09-227-357-553
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SOFTWARE: Patentin '
SEQ ID NO 553
LENGTH: 55
TYPE: PRT
Sequence 552, Application US/09227357
Sequence 56342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
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ER FILING DATE: 1997-08-18
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ER APPLICATION NUMBER: 60/055,949
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,953
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ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,950
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,947
ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,964
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ER FILING DATE: 1997-08-18
ER APPLICATION NUMBER: 60/055,964
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FILING DATE:
APPLICATION A
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FILING DATE:
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FTILING DATE: 1997-09-12
OF SEQ ID NOS: 672
E: Patentin Ver. 2.0
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,928
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APPLICATION NUMBER: 60/051,920
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,733
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Pred. No. 37;
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EARLIER FILING I
NUMBER OF SEQ II
SOFTWARE: Patent
SEQ ID NO 552
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                                                               PR FILING DATE: 1997-08-18
R APPLICATION NUMBER: 60/058,785
RR FILING DATE: 1997-09-12
RR APPLICATION NUMBER: 60/058,664
RR FILING DATE: 1997-09-12
RR APPLICATION NUMBER: 60/058,660
RR FILING DATE: 1997-09-12
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APPLICATION NUMBER: 60/055,953
TTITING DATE: 1997-08-18
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APPLICATION NUMBER: 60/051,931
APPLICATION NUMBER: 60/051,931
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FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/052,795
FILING DATE: 1997-07-08
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APPLICATION NUMBER: 60/052,733
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APPLICATION NUMBER: PCT/US98/13684
FILING DATE: 1998-07-07
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552
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                                     NUMBER: 60/058,
1997-09-12
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                                                                                                                      RESULT 10
US-09-361-707-42
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                                                                         Sequence 42, Application US/09361707 Patent No. 6258937 GENERAL INFORMATION:
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                             Query Match
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIR
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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TELEFAX: 200154
                                                                                                                                                                                      165 ESRTGD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/683,262B
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                              Local Similarity
hes 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: rish Compress: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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STATE: Massa
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Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR NUMBER OF SEQUENCES: 117
                                                        APPLICANT: Tong, Shuping
                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts
                                                                                                                                                                                                                                                                                                                                                                       174 amino acids
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83.3%;
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83.3%;
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                                                                                                                                                                                                                                              1; Mismatches
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Pred. No.
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Pred. No. 1.2e+02;
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US-08-462-481-5
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                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5840577
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5,
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                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hassel, Brew APPLICANT: Zhou, Aimin TITLE OF INVENTION: And TITLE OF INVENTION: End
                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 ESRTGD 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.0%;
Local Similarity 83.3%;
les 5; Conserva+***
                                                                                                                                                                                     COUNTRY: U
                                    FILING DATE:
                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                          STATE:
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                                                                                                                                                                                                                                                                                               ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
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APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/683,262 FILING DATE: 18-JUL-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                     5840577
                                                                                                                                                                                                                        Florida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                            200 East Broward Boulevard
                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                Hassel, Bret A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silverman, Robert H.
                                                                                                                                                                                                                                                                                Russel
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                                                      US/08/462,481
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Pred. No. 1.2e+02;
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Query Match
Best Local Similarity
Thehes 5; Conserve
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TELEPAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                         APPLICATION NUMBER: US 08/198,973
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: MADSO, Peter J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-16
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                      TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu Transgenic Plants, Vectors
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                   TOPOLOGY:
                                                                                                                                             TELEPHONE: 305/527/2498
                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                      LENGTH:
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200 E. Broward Boulevard
                                                                      190 amino acids
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linear
                   linear
protein
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71.4%;
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Pred. No. 1.3e+02;
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US-08-487-797-7
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                                                                                   Sequence 7, Application US/08487797 Patent No. 5866787
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08434998 Patent No. 5866781
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Best Local
GENERAL INFORMATION:
APPLICANT: Silverman, Robert H.
APPLICANT: Sengupta, Dibyendu N.
TITLE OF INVENTION: Transgenic F
TITLE OF INVENTION: Functional H
                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 305/527/2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Manso, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Silverman, Robert H.
APPLICANT: SenGupta, Dibyendu N.
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
TITLE OF INVENTION: Cells and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 200 E. Broward
CITY: Fort Lauderdale
STATE: Florida
                                                                                                                                                                                       58 EKARTAD
                                                                                                                                                                                                                                                                                                                                                   LOBOTOCK:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Manso, Peter J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 EKARTAD
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                     1 EKSRTGD 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33301
                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 E. Broward Boulevard
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                   75.0%;
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71.4%;
 Functional Human 2-5A System
                   Transgenic Plants Co-Expressing A
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                                                                                                                                                                                                                                                                   Score 27; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27; DB 2;
Pred. No. 1.3e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                  Length 190
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RESULT 15
US-08-701-005A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08701005A Patent No. 5877019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 305/463-2030
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: 555 - 13th Street, N.W., Suite 701 E
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION: tent No. 5877019
                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                     ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MANSO, PETER J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 305/468-7811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/487,797 FILING DATE: 07-JUNE-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Holland & Knight
STREET: One E. Broward Boulevard, #1300
CITY: Fort Lauderdale
                                   APPLICATION NUMBER: US/O FILING DATE: 21-AUG-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 EKARTAD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 33301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EKSRTGD 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                   Hassel, Bret A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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Encoding Sequence Therefor
 US 08/141,304
                                                                     US/08/701,005A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB 2;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 190;
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Query Match
Best Local Similarity
Thes 5; Conservat
Search completed: November 12, 2002, 17:01:41 Job time: 1.96137 secs
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                                                                                                                                                                                      US-08-701-005A-5
                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                              58 EKARTAD 64
                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                            1 EKSRTGD 7
                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                             Jondle, Robert J.
Jondle, Robert J.
33,915
                                                                                                                                                                                                                                                                                                        190 amino acids
                                                                                                                                                                                                                                                                                                                                                          202-783-6031
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                            single
                                                                                                                                        75.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/028,086
                                                                                                                        Score 27; DB 2; Length 190; Pred. No. 1.3e+02; 1; Mismatches 1; Indels
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Gaps

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Database
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            November 12, 2002, 17:00:26; Search time 0.540773 Seconds (without alignments) 186.540 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	17	16	15	14	13	12	11	10	9	8	7	6	· vi	4	w	2		Result
26	27	27	27	27	27	27	27	27	27	2 7	27	28	28	28	31	31	36	Score
72.2	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	77.8	77.8	77.8	86.1	86.1	100.0	Query Match
680	2568	855	650	590	394	394	382	359	174	144	54	762	466	50	646	639	181	Length
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	DB
US-09-864-761-46399	US-09-866-108-3	US-09-815-242-11930	US-09-943-671-29	US-09-943-671-25	US-09-946-034-2	US-09-863-475A-4	US-09-825-414-30	US-09-994-427A-11	US-09-818-066-42	US-09-815-242-11116	US-09-867-550-1596	US-09-925-299-998	US-09-741-669-303	US-09-864-761-37990	US-09-815-242-12304	US-09-815-242-5390	US-09-854-864-5	ID
Sequence 42165, A Sequence 46399, A		Sequence 11930, A	Sequence 29, Appl	Sequence 25, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 30, Appl	Sequence 11, Appl	Sequence 42, Appl	Sequence 11116, A	Sequence 1596, Ap	Sequence 998, App	Sequence 303, App	Sequence 37990, A	Sequence 12304, A	Sequence 5390, Ap	Sequence 5, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	26	0.0
72.2								72.2				72.2			72.2	72.2	72.2	72.2		72.2			72.2	72.2	12.2
876	874	766	760	742	469	426	372	315	315	307	283	264	258	241	241	241	240	234	212	199	174	174	174	174	1/0
10	10	10	10	10	10	10	10	10	10	10	9	10	10	12	10	10	10	10	10	10	10	10	10	10	Ţ
US-09-815-242-10269	US-09-815-242-11809	US-09-795-693-17	US-09-265-606-2	US-09-799-777-18	US-09-925-300-1494	US-09-864-761-42921	US-09-818-066-64	US-09-904-615-124	US-09-739-254-124	US-09-788-626-20	US-09-970-989-2	US-09-925-301-905	US-09-921-640-9	US-10-116-378-3	US-09-915-593-28	US-09-915-593-4	US-09-915-593-6	US-09-915-593-2	us-09-925-299-968	-92	US-09-818-066-48	US-09-818-066-47	US-09-818-066-46	US-09-818-066-45	4
	Sequence 1	Sequence 1	Sequence 2	Sequence 1	Sequence 1	_	Sequence 6.			Sequence 2	Sequence 2,	Sequence 9		Sequence 3	Sequence 2	Sequence 4	Sequence 6,	Seguence 2			Sequence 4	Sequence 4	Sequence 46	Sequence 4	Sequence 4
10269, A	11809, A	17, Appl	, Appli	18, Appl	1494, Ap	2921, A		124, App		20, Appl	Appli	905, App	9, Appli	Appli	28, Appl	, Appli	-	Appli		Appli	48, Appl	-	6, Appl	•	•

ALIGNMENTS

US-09-854-864-5

Sequence 5, Application US/09854864 Patent No. US20020081296A1

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RESULT 2
US-09-815-242-5390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-854-864-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5
LENGTH: 181
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG

APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE REFERENCE: A-6868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR TILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-27

NUMBER OF SEQ ID NOS: 31

COCTUMENT DETAILS OF SEC ID NOS: 31
Sequence 5390, Application US/09815242
PATENT NO. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                              102 EKSRTGD 108
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                                  PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
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LENGTH: 639
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CURRENT FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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APPLICANT:
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PRIOR TILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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PRIOR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
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Xu, H. Howard
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US-09-815-242-12304
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LENGTH: 646
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Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 37990
LENGTH: 50
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PRIOR APPLICATION NUMBER: US 09/632,366
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TYPE: PR
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                  TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                       APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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                                                                                                                  APPLICATION NUMBER: US 09/774, 203
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Chen, Wensheng
                                                                                                     DATE:
                                                                                NATE: 2001-01-29
ID NOS: 49117
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1909-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 998
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Best Local Similarity
Thes 5; Conserv
                                                      ; TYPE: PRT; ORGANISM: Homo sapiens US-09-925-299-998
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: Proliferation of E. coli
FILE REFERENCE: ELITRA.0094
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEG ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-925-299-998
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US-09-741-669-303
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US-09-741-669-303
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                                                                                                         LENGTH: 762
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EXPRESSED IN FETAL LIVER, SIGNAL = 0.57
EXPRESSED IN LUNG, SIGNAL = 0.65
EST_HUMAN HIT: AU156079.1, EVALUE 2.20e+00
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71.4%;
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Pred. No.
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Pred. No.
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   DB 10;
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Query Match
Best Local Similarity
Watches 5; Conserve
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                                   CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells a
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Leach, APPLICANT: Mehra
                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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  APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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Law, Debbie
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                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D. Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall,
                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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2000-12-22
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Pred. No.
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Query Match
Best Local Similarity
5; Conserv
RESULT 10
US-09-994-427A-11
; Sequence 11, Application US/09994427A
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US-09-818-066-42
; Sequence 42, Application US/09818066
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SOFTWARE: FastSEQ for
SEQ ID NO 11116
LENGTH: 144
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INFORMATION FOR SEQ ID NO: 42:
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                                                                                   165 ESRTGD 170
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les 5; Conserv
                                                                                                                  2 KSRTGD 7
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                              MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/818,066 FILING DATE: 27-Mar-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
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83.3%;
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                                                                                                                                              ; Score 27; DB; Pred. No. 54; .1; Mismatches
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Pred. No.
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Query Match
Best Local Similarity
Warches 5; Conserv
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Best Local Similarity
Watches 5; Conserva
                                                                                                                                                                         US-09-863-475A-4
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US-09-994-427A-11
                                                                                  Sequence 4, Application US/09863475A
Patent No. US20020102688A1
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 11
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AIPLICANT: Schiff, J. Michael
TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
FILE REFERENCE: 083,002
CURRENT APPLICATION NUMBER: US/09/994,427A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 60/253,395
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/224,604
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/249,548
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/825,414
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/194,160
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES FILE REFERENCE: 19603/3243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Collmer, Alan
APPLICANT: Alfano, James R.
APPLICANT: Charkowski, Amy O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 17
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                            197 EKGRAGD 203
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TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
OF GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382
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71.4%;
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Pred. No. 1.2e+02;
Pred. No. 2;
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Pred. No. 1 le+02;
                                                                                                                                                                                                                                                                                                                                                                                    Length 382;
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RESULT 13
US-09-946-034-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09946034 Patent No. US20020152488A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 2363-060-55
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEY 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/863,475A
APPLICATION NUMBER: US/09/863,475A
FILING DATE: 24-May 2001
CLASSIFICATION: -dinknown>
PRIOR APPLICATION NUMBER: 07/914,281
APPLICATION NUMBER: 07/914,281
FILING DATE: 20-JUL-1992
ATTROBUREY/ACCENT INCOMMATION:
ZIP: 30309-4530

ZIP: 30309-4530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/946,034

FILING DATE: 04-Sep-2001

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 EKGRNGD 104
                                                                                                                                                                                                                                                                                                                                                                KOTEN, EUGEN
TITLE OF INVENTION: GENETICALLY ENGINEERED ANIMALS FOR USE
AS ORGAN DONORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lavalleye, Jean-Paul M. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cooper, David K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKSRTGD 7
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                                                                                                                                                                                                                                                                      STREET: 1100 Peachtree Street, Suite 2800 CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                 STATE: GA
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Patrea L. Pabst
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71.4%;
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Pred. No. 1.2e+02;
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                                                                                           Version #1.25
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RESULT 15
US-09-943-671-29
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: Sequence 29, Application US/09943671
: Patent No. US20020106733A1
: GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
                                                                                                                                                                                           Matches
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                                                                                                                                                                                                            Best
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/943,671
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/232.191
PRIOR FILING DATE: 1999-10-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/110,941 PRIOR FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David
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SEQUENCE CHARACTERISTICS:
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                                                                                                                       450 KDRTGD 455
                                                                                                                                                                                         Local Similarity hes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (404)-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/049,817 FILING DATE: 20-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 394 amino acids
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Pred. No. 1.2e+02;
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Pred. No.
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APPLICANT: Stahl, Andreas

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APPLICANT: Hirsch, David J.

APPLICANT: Lodish, Harvey F.

TITLE OF INVENTION: Fatty Acid Transport Proteins

FILE REFERENCE: WHI97-21p3ME

CURRENT APPLICATION NUMBER: US/09/943,671

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/232,191

PRIOR APPLICATION NUMBER: 09/232,191

PRIOR FILING DATE: 1999-10-14

PRIOR APPLICATION NUMBER: 60/210,941

PRIOR APPLICATION NUMBER: 60/110,941

PRIOR FILING DATE: 1998-12-04

INMBER OF SEQ ID NOS: 37

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 29

SEQ ID NO 29

CONTROL FILING DATE: 1998-12-04

SEQ ID NO 29

CONTROL FASTSEQ FOR WINDOWS VERSION 3.0

PRIOR APPLICATION NUMBER: 60/110,941

PRIOR APPLICATION NUMBER: 60/110,941

PRIOR FILING DATE: 1998-12-04

SEQ ID NO 29

SEQ ID NO 29

CONTROL FASTSEQ FOR WINDOWS VERSION 3.0

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Perfect score:
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1 EKSRTGD 7
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

A; Molecule type: DNA A; Residues: 1-184 <LAA>

A; Status: preliminary

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	æ	7	თ	U	4	w	2	-	Result No.
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421	415	412	378	371	324	321	288	128	121	115	111	1031	583	316	149	526	463	450	396	160	92	1195	646	1361	1163	862	585	184	Length
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hypothetical prote	alpha-methylacyl-C	hypothetical prote	chain a, crystal s	hate transp		hypE protein - Bra	0	etical	hypothetical prote		pr		ABC transporter (A	hypothetical prote	ribosomal protein	L-galactonolactone	astB/chuR-related	probable kasein ki	trai	hypothetical prote	transcription regu		prot		lirected	protein hom	ABC transporter (A	B-cell maturation	Description

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type I restriction	hypothetical prote	hypothetical prote	ABC excision nucle	copper-transportin	hypothetical prote	conserved hypothet	zinc finger protei	afamin precursor -	selenocysteine tRN	hypothetical prote	ABC transporter (A	55.5K sporulation	mannose-1-P guanos	mannose-1-P guanos	hypothetical prote

ALIGNMENTS

N;Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: \$43486; \$31208; \$38661
R;Laabl, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bid
A;Reference number: \$43486; MUID:94218235; PMID:8165126
A;Accession: \$43486

B-cell maturation factor - human

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ABC transporter (ATP-binding protein) homolog yheI - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001 C;Accession: A69829 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azeved
                                                                                                                              RESULT
A69829
                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GDB:135977; OMIM:109545
A:Map position: 16p13.1-16p13.1
A:Introns: 44/1: 93/1
C:Superfamily: human B-cell maturation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245 R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi EMBO J. 11, 3897-3904, 1992
                                                                                                                                                                                                                              ₽
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A;Molecule type: mRNA
A;Residues: 4-184 <LA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Accession: S31208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB:BCMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z14955
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A; Residues: 1-184 <LA2>
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Best Local
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Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

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lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Holsono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pobl, T. M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sarot akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aluthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Reference number: A09580; MUID:98044033; PMID:9384377
RESULT 4
S07137
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A;Experimental source: strain 168
C:Genetics:
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                                                                                                                                                                                                                                                                                        A:Start codon: TTC
C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2
C:Keywords: chloroplast
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A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene
A;Reference number: A38013
A;Reference number: A38013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: cv. R; Shinozaki, K.; Ohme, M.; Deno, H.; Kamogashira, T.; EMBO J. 5, 2043-2049, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpoC protein homolog - common tobacco chloroplast
C;Species: chloroplast Nicotiana tabacum (common tobacco)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_
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Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, A; Authors: Tourger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, A; Authors: Tourger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, A; Authors: Tourger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, A; Authors: Tourger, D.; Funa, A; Hilbert, H.; Holsappel, S.;
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                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics
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A; Residues: 1-862 <SUG>
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                                                                                                                                                                                                                                                                                                                                                                        A; Genome: chloroplast
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Best Local
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nes 6; Conserv
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                                                                                                EKSRSGD 615
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85.7%;
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Tanaka, M.; Waki
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Pred. No. 47;
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Kusuda, J.; Takaiwa, F.;
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Kato, A.; Tohdoh,
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C; Keywords:
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                                                A; Molecule
                        A; Residues:
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DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - garden pea chloroplast C;Speciles: chloroplast Pisum sativum (garden pea) C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1999 C;Accession: S07137
                                                                                                                                        C;Accession: H89843

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kalto, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Residues: 1-1163 <COZ>
A;Cross-references: EMBL:X03912; NID:g12137; PIDN:CAA27545.1;
                                                                                                                                                                                                                                                                                                                                                  C;Species: Staphylococcus aureus
C;Date: 10-May-2001 *sequence_revision 10-May-2001 *text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SA0674 [imported] - Staphylococcus aureus (strain N315) C; Species: Staphylococcus aureus
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A; Residues: 1-1361 < HUD>
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A;Title: Pea chloroplast DNA encodes homologues of Escherichia
A;Reference number: S07137; MUID:86323089; PMID:3530249
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                                                                                      A; Status: preliminary
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                               1-646 <KUR>
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GB:BA000018; PID:g13700610; PIDN:BAB41907.1;
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence aumber: A86141; MUID:21016719; PMID:11130712
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                             A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; PMID:11743193
A;Accession: AB3173
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Karp, P.; Romero, P.; Zhang, S.
Science 394, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AB3173
C;Accession: AB3173
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; L1, M.; McClelierage, G.; Gillet, M.; Gillet, M.; Gillet, M.; Gillet, M.; Gillet, M.; Gillet, W.; Gillet, M.; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F16M22.3 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Date: 05-Mar-2001 #sequence_revision 05-Mar-2001 #text_change 31-Mar-2001 C;Accession: E96615
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C; Superfamily:
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                                                                      A;Cross-references: GB:AE008687; PIDN:AAL45803.1; PID:g17743541; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-92 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                              A; Authors: Yoo, H.; Tao, ster, E.W.
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A; Residues: 1-1195 <STO>
A;Gene: Atu5113
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; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, I
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative
A;Reference number: AD3232; PMID:11756888
A;Accession: AH3650
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A;Map position: I
C;Keywords: glyco:
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A;Molecule type: DNA
A;Residues: 1-396 <KUR>
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A; Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
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C;Accession: C97289
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2.7.1.-) - Arabidopsis thaliana F20B18.210
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P.H.; Hagius, S.; O'Callaghan, I
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RESULT 12
E72268
astB/ChuR-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-un-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: E72268
C;Accession: E72268
C;Accession: E72268
C;Accession: Picket, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, R.A.; Right, R.A.; Ri
                                                                                                                                                           L-galactonolactone oxidase (EC 1.1.3.24) - yeast (S N;Alternate names: D-arabinono-1.4-lactone oxidase; C;Species: Saccharomyces cerevisiae C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 C;Accession: S49641; S61944 R;Gentles, S.; Bowman, S. submitted to the EMBL Data Library, November 1994 A;Reference number: S49627
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S49641
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A;Note: F20618.210
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase
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A;Experimental source: cultivar Columbia; BAC clone F20B18
C;Genetics:
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C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 14-Sep-2001
C;Accession: T04265
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15263
A;Accession: T04265
A;Cross-references: EMBL:Z46660; NID:g575702; PID:g575717; MIPS:YML086c R;Huh, W.K.; Kim, S.T.; Kim, J.Y.; Hwang, S.W.; Kang, S.O. submitted to the EMBL Data Library, November 1995
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A; Residues: 1-463 <ARN>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: E72268
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                                                                                                    A; Molecule type: DNA
A; Residues: 1-526 <GEN>
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A; Residues: 1-450 <BEV>
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Best Local
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5; Conserv
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ce: strain MSB8
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pela, D.; Chain, P.; Cowie, A.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
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C;Date: 08-May-1998 *text_change 13-Aug-1999
C;Date: 08-May-1998
C;Accession: H70441
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Gral
                                       A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-H
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher,
                                                                                                                                                                                                          A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A;Reference number: A95262; MUID:21396509; PMID:11481432 A;Accession: E95307
                                                                                                                                                                                                                                                                           R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, ; Kalman, S.; Keeting, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Proc. Natl. Acad. Sci. U.S.A. 98, 983-9888, 2001
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C; Superfamily:
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A; Residues: 1-149 < AQF>
A; Cross-references: GB:
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C;Reywords: ascorbic acid biosynthesis; oxidoreductase;
F;172-188/Domain: transmembrane #status predicted <TMM>
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C;Accession: E95307
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A; Map position: 13L
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A; Residues: 1-526 < HUH>
                                                                                                            A;Cross-references: GB:AE006469; PIDN:AAK65023.1; PID:g14523453; GSPDB:GN00165
                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-316 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SMa0689 [imported] - C; Species: Sinorhizobium meliloti
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A; Accession: S61944
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Z143_HUMAN
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UVRC_STRCO
ITA1_HUMAN
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RL15_HAEIN
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EMBL; 229775; CAA82691.1; -.
EMBL; 225774; CAA82690.1; -.
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Boyle W.J., Sarosi I., Hau H., Senaldi G., Theill L.
"APRIL and TALL-I and receptors BCMA and TACI: syste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "TACI and BCMA are receptors autoimmune disease.";
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                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the European Bioinformatics institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION, AND INTERACTION WITH APRIL MEDLINE-21170294; PubMed-10973284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20259066; PubMed-10801128; Gross J.A., Johnston J., Mudri S.,
                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "APRIL and TALL-I and receptors humoral immunity.";
                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 404:995-999(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type III membrane protein. and perinuclear Golgi-like structures.
TISSUE SPECIFICITY: Expressed in mature B-cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 THER-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cells or monocytes.
DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humoral immunity. Activates NF-kappa-B and JNK. SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
PUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL
Promotes B-cell survival and plays a role in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZED BY A CHROMOSOMAL WHICH INVOLVES BCMA AND IL2.
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                                                                                                       CYTOPLASMIC (POTENTIAL)
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277AF11E2767D932 CRC64;
                                                                                          BREAKPOINT FOR TRANSLOCATION
                                                                                                                                 (POTENTIAL).
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                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
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P12227;
01-OCT-1989
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01-0CT-1989
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16-0CT-2001
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RPOD_SPIOL
                                                                                                                                                                                                        Pfam; PF01854; RNA_pol_A2; 2.
Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-86323089; PubMed-3530249;
Cozens A.L., Walker J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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  DNA-directed
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RESULT 4

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OS Arabid
OG Chloro
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P56764;
30-MAY-2000
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16-OCT-2001
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassloales; Brassloaceae; Arabidopsis.
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PIR; A29959; A29959.
HSSP; Q9KWUG; 1HQM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The plastid chromosome of spinach (Spinacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmitz-Linneweber C., Maier R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Geant d'hiver, and cv. MEDLINE-21187424; PubMed-11292076;
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MEDLINE=88316931; PubMed=3045324;
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
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Pro; IPR002879; RNA_pol_A2.
PF00623; RNA_pol_A; 1.
PF01854; RNA_pol_A2; 2.
PF01854; RNA_pol_A2; 2.
PF02854; Transcription; DNA-directed RNA polymerase;
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InterPro; IPR002879; RNA_pol_A?
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
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Sato S., Nakamura Y., Kaneko T., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
STRAIN-cv. Columb
                                                                                          "The multisubunit chloroplast RNA polymerase A from mustard (Sinapis alba L.). Integration of a prokaryotic core into a larger complex with organelle-specific functions.";
Eur. J. Blochem. 267:253-261(2000).
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTIC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Sinapis. NCBI_TaxID-3728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                       STRAIN-cv. Albatros; TISSUE-Cotyledon; MEDLINE-20069369; PubMed-10601874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sinapis alba (White mustard) (Brassica hirta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPOC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-directed
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                                                                                                                                                                                                                                                                Pfannschmidt T.,
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 6-20.
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                                         SUBSTRATES CATALYTIC ACTIVITY: N nucleoside
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \{RNA\}_{\{N\}}. SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: N nucleoside triphosphate
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HSSP; OSKWUG: HOM.

InterPro; IPR000772; RNA_pol_A.

InterPro; IPR002879; RNA_pol_A2.

Pfam; PF00623; RNA_pol_A2; 1.

Pfam; PF01854; RNA_pol_A2; 1.

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Transferase; 1384 AA; 157740 MW;
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01-0CT-1994
16-0CT-2001
                                                                                                                                                                                                                                                                  Olmstead R.G., Sweere J.A., Wolfe K.H.;

"Ninety extra nucleotide in ndhr gene of tobacco chloroplast DNI
summary of revisions to the 1986 genome sequence.";

Plant Mol. Biol. 22:1191-1193(1993).

-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCI
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamaguchi-Shinozaki K., Ohto C., Torazawa K., )
Deno H., Kamogashira T., Yamada K., Kusuda J.,
Tohdoh N., Shimada H., Sugiura M.;
"The complete nucleotide sequence of the tobaccity gene organization and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-cv. Bright Yellow 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinozaki K., Ohme M., Tanaka M., Wakasugi T., Ha
Matsubayashi T., Zaita N., Chunwongse J., Obokata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
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                                                                                                                                  SUBUNITS: ALPHA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNITS: ALPHA, BETA, BETA', AND BETA"
                                                                                                                                                                                                                                              SUBSTRATES
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                                                                                                                                                                                          (RNA)(N).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE O STRAIN-ATCC 24858 / WHIO1; MEDLINE-99140446; PubMed=10094636; Huh W.-K., Lee B.-H., Kim S.-T., K Hwang C.-S., Lee J.-S., Kang S.-O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produ
between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                        Gentles S., Bowman S., Barrell B.G., Rajanureum R., Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
D-arabinono-1,4-lactone oxidase (EC 1.1.3.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   1,4-LACTONE AND L-GALACTONO-1,4-LACTONE.
-!- CATALYTIC ACTIVITY: D-arabinono-1,4-lactone
ascorbate + H(2)0(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "D-Erythroascorbic acid is an important Saccharomyces cerevisiae."; Mol. Microbiol. 30:895-903(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma-lactone oxidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P54783; 042618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 200044; CAA77410.1; ALT_SEQ.
HSSP; Q9KWU6; 1HQM.
InterPro; IPR000722; RNA_Pol_A.
InterPro; IPR002879; RNA_Pol_A2.
                                                                                                                                                                                                                                                                                                -!- FUNCTION: CAN OXIDIZE L-GULONO-1,4-LACTONE AS WELL AS D-ARABINONO-
                                                                                                                                                                                                                                                                                                                                                        STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-lactone oxidase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALO1 OR YML086C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALO_YEAST
                                                                                                                                                                                                                      -!- COFACTOR: FAD.
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                                                                                                                                      PTM: The N-terminus is blocked.
SIMILARITY: Belongs to the oxyg
                                                                                                                                                                            PATHWAY: D-erythroascorbic acid bios: SUBCELLULAR LOCATION: Mitochondrial.
                                                                                                                   oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKSRTGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kang S.-O.;
                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۳.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic sequence encoding L-galactono-
                                                                                                                                                                                               acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                        oxygen-dependent FAD-linked
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                                                                             It is produced through
                                                                                                                                                                            biosynthesis; final starial. Membrane-embedded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86-105 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y.-R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhie G.-E., Baek Y.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ALO) (L-galactono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1388
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RESULT 8

RPOD_GUTH
ID RPOD_G
AC 078483
DT 15-DEC
DT 15-
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                                                                       EMBL; Arva...
HSSP: Q9KWU6; 1HQM.
InterPro: IPR000722; RNA_pol_A.
InterPro: IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Pfam; PF01854; Transcription; DNA-directed RNA polymerase;
PF01854; RNA_pol_A2; 2.
Pfam; PF01854; RNA_pol_A2; RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998
15-DEC-1998
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common ancestry with red algae.";
J. MOI. EVOI. 48:236-244(1999).
-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99128221; PubMed=9929392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Cryptophyta; Cryptomonadaceae;
NCBI_TaxID=55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guillardia theta Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-directed RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR001575; Oxid_FAD_bind.
Pfam; PF01565; FAD_binding_4; 1.
PROSITE; PS00862; OX2_COVAL_FAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBSTRATES.
-1- CATALYTIC ACTIVITY: N nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Douglas S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
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les 6; Conser
                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EKSRTGD 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RNA)(N).
SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA, BETA', AND BETA'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; AB009401; BAA23804.1;
; Z46660; CAA86652.1; -.
$0004551; ALO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKSSTGD 299
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Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long as
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526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 38, Last annotation update)
d RNA polymerase beta* chain (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59493 MW;
                              83.3%;
71.4%;
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85.7%;
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FAD (COVALENT) (BY SIMILARITY).
A -> P (IN REF. 2).
                              Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             942177A74A738EC8 CRC64;
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                                  1e+02;
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RESULT 10
RPOD_MESULT 10
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OT RPOC_2
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Q9MUS7;
16-OCT-2001
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16-OCT-2001
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RL15_AQUAE
Mesostigmatales;
NCBI_TaxID=41882;
[1]
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PROSITE; PS00475; RIBOSOMAL_L15; FALSE_NEG.

RIDOSOMAl protein; rRNA-binding; Complete proteome
SEQUENCE 149 AA; 16572 MW; 12BBDA4E92D90357 CR
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Pfam; PF01305; Ribosomal_L15; 1.
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-!- FUNCTION: THIS PROTEIN
(BY SIMILARITY).
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                                                  Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
                                                                   Chloroplast
                                                                                      Mesostigma viride
                                                                                                                     DNA-directed
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(Rel. 39,
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d RNA polymerase beta" chain (EC 2
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                                Mesostigmataceae;
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71.4%;
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Pred. No.
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Mismatches
                                   Mesostigma
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RESULT 11
RPOM_YEAST
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Best Local S
Matches
                                    STRAIN=S288C / AB972;
MEDLINE=95400292; PubMed=7670463;
Murakami Y., Naktou M., Hagiwara H., Sh
Sasanuma S.-I., Sasanuma M., Tsuchlya Y
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Crested)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase, mitochondrial pr
RPO41 OR YFL036W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
HSSP;
                                                                                                                                                                                   MEDLINE-88002333; PubMed-3308116; MEDLINE-88002333; PubMed-3308116; Masters B.S., Stohl L.L., Clayton D.A.; "Yeast mitochondrial RNA polymerase is bacteriophages T3 and T7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 2.
Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
SEQUENCE 1223 AA; 138048 MW; 4044E90805FC472A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILING ... Offis C., Turmer m.;
Temieux C., Offis C., Turmer m.;
Tancestral chloroplast genome in Mesostigma
Tancah of green plant evolution.";
                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacci
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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P13433;
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                                                                                                                                              SEQUENCE FROM N.A
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CATALYTIC ACTIVITY: N nucleoside triphosphate -
 FUNCTION:
OF DNA INT
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5; Conser
10:261-268(1995).
N: DNA-DEPENDENT REINTO RNA USING THE
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a Y., Soeda
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CATALYZES THE TRANSCRIPTION LEOSIDE TRIPHOSPHATES AS
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EMBL: D50617; BAA03203.1; ...
PIR; A27336; A27336.
HSSP; P00573; 1ARO.
SGD; S0001858; RP041.
SGD; S0001858; RP041.
InterPro; IPR002092; RNA_pol_phage.
Pfam; PF00940; RNA_pol; 1.
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15-JUL-1998
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ACT_SITE
ACT_SITE
ACT_SITE
                                        Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothler B., Olu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                     J. Bacteriol.
-!- FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota;
Methanobacteriaceae; Me
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PROSITE; PS00489; RNA_POL_PHAGE_2; 1.
Transferase; DNA-directed RNA polymerase;
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SUBCELULAR LOCATION: Mitochondrial
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vrv protein P-II 1.
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YCW1_YEAST
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YCR071C OR YCR71C.
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PRODOM; PD001194; PII_G1nB; 1.

PROSITE; PS00638; PII_GLNB_CTER; 1.

Transcription regulation; Nitrogen fixation; Complete proteome.

SEQUENCE 115 AA; 12904 MW; 4E77B0AEA979BA53 CRC64;
                                                                                                                                                                                                                                                                                                                  EMBL; X59720; CAA42269.1; PIR; S19486; S19486.
                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1992) to the EMBL/GenBank/DDBJ -1- SIMILARITY: SOME, TO S.POMBE SPAC3H8.03.
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Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetacese; Saccharomyces.
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                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 121 AA; 13682 MW; F8E3304D6F38475A CRC64;
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een the Swiss Institute of Bioinformatics
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COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                 STRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv2898c.
RV2898C OR MT2966 OR MTCY274.29C.
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01-0CT-1996
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EMBL; AE007119; AAK47292.1; ALT_INIT.
TIGR; MT2966; -.
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NCBI_TaxID=1773;
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Pred. No. 22;
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Search completed: November 12, 2002, 16:58:59 Job time: 1.60086 secs
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MEDLINE-87002480; PubMed-3019562;

MEDLINE-87002480; PubMed-3019562;

Lacks S.A., Mannarell1 B.M., Springhorn S.S., Greenberg B.;

"Genetic basis of the complementary DpnI and DpnII restriction systems of S. pneumoniae: an intercellular cassette mechanism.";

Cell 46:993-1000(1986).
                                                                                                                                                                                                                                                                                EMBL; M14339; AAA88582.1; -.
PIR; B24372; B24372; B25372.
REBASE; 777; DpnII.
Hydrolase; Endonuclease; Nuclease; Restriction system.
Hydrolase; Endonuclease; Nw; F7346EEA6940EB33 CRC64;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Type II restriction enzyme DpnII (EC 3.1.21.4) (Endonuclease DpnII)
(R.DpnII).
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83.3%;
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SPTREMBL_21:*

1: sp_archea:*
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4: sp_numan:*
5: sp_inverteb
6: sp_mamal:*
7: sp_mhc:*
10: sp_phage:*
11: sp_rodent:
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Q939S3	Q939S5	Q939S6	Q9VKI2	Q8ZVW5	Q9AEG9	Q9AC93	Q9AC94	Q9AEH0	Q9ACF1	09ACF2	Q9ACF3	Q9ACF4	Q9AEH3	099072	Q8UZ27	8xx660	Q8R5D1	Q8x050	Q936Y8	Q9X143	046078	Q9SZI1	Q91BP9	Q917x6	. Q8YAX2	Q91TF2	Q91TF3	Q8RUB2
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EMBL; Z99109; CAB12810.1; -.
HSSP; P13569; INBD,
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001140; ABC_transportr.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00064; ABC_transportr.
Pfam; PF00065; ABC_tran; 1.
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Probom; Pb000006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
SMART; SM00321; ABC_TRANSPORTER; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding: Hypothetical protein; Transport; Complete proteome ATP-binding: AA; 65111 MW; AB82FA64338F8161 CRC64;
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                                                                                                                                                                                                                                                                                                             PubMed=11792842;
PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima
Shiba T., Ogasawara N., Hattori M., Kuhara Shiba T., Ogasawara sequence of Clostridium pe
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Bacteria; Firmicutes; Bacillus,
Clostridiales; Clostridiaceae;
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Submitted (NOV-1997) to
-!- SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8XL40
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                        L; AP003189; BAB80908.1; ... appro; IPR001757; ATPASS_E1-E2. appro; IPR004014; Cation_ATPASS_erpro; IPR004014; Cation_ATPASS_serpro; IPR001454; Hlgnass/hydrlass_appro; IPR001245; Tyr_pkinass_appro; IPR001245; Tyr_pki
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Cation_ATPase_C; 1
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85.7%;
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TO THE ATP.BINDING TRANSPORT PR
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                                         A Harris N.L. Harvey D., Helman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
A Jalali M., Kalush F., Karpen G.H., KE Z., Kennison J.A., Ketchum K.A.,
A Kimmel B.E., Rodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lisko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
A Lisko P., Lei Y., Levitsky A.A., Li J., Mcherson D.,
A Mchalov G., Milshina N.V., Mobarry C., Mcheod M.P., Mcherson D.,
A Mchalov G., Milshina N.V., Mobarry C., Mcheod M.P., Mcherson D.,
A Merkulov G., Milshina N.V., Mobarry C., Mcheod M.P., Mcheof D.L.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Nelson D.R., Nixon K., Nixon K., Nusskern D.R., Pacleb J.M.,
A Nelson D.R., Nixon K., Saunders R.D.C., Scheeler F., Shen H.,
A Nelson D.R., Pattum G.S., Pan S., Pollard J., Purl V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
A Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
A Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Sheng X.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhong L.,
A Sheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
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Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zl
Glbbs R.A., Myers E.W., Rubin G.M., Venter J
"The genome sequence of Drosophila melanogas
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NCBI_TaxID-7227;
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PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
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A., Galle
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                              Lotus japonicus.
Chloroplast.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
NCBI_TaxID-34305;
                                                                                                                                                                                                                                                                           O9BBS7 PRELIMINARY; PRT; 1332 AA.
O9BBS7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
RNA polymerase beta' subunit-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
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Bukaryota; Mctazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc.

Ephydroidea; Drosophilidae; Drosophila.
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DNA Res. 7:323-330/2000
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MEDLINE-21082929; PubMed-11214967;
Kato T., Kaneko T., Sato S., Nakam
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Eucenothera plastomes.";
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Chiu W.L., Sears B.;
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STRAIN=ACCESSION MG-20;
1134
                                                                                                                                                             Chloroplast SEQUENCE 1
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InterPro; IPR002879; RNA_pol_A2
                                                                                                                                                                                                                                            InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2
                                                                                                                                                                                                                                                                                                        Mol. Gen. Genet. 263:581-58
EMBL; AJ271079; CAB67153.1;
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                                                                                                                                                                                                                                                                                         HSSP; Q9KWU6; IHQM.
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082969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabacum with emphasis microevolution."; Submitted (MAY-2000) to the EMBI EMBL; AJ316582; CAC88034.1; -. SEQUENCE 1389 AA; 156857 MW;
                                                                                                                                       InterPro; IPR000238; Rib_bind_factA. Pfam; PF02033; RBFA; 1. SEQUENCE 132 AA; 15102 MW; 24BCF
                                                                                                                                                                   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; AF348330; AAK31156.1; -
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01-JUN-2002 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
RNA polymerase beta II subunit.
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01-JUN-2002
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01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
A2-5a orf1 (Fragment).
Bacillus Sp.
Bacteria, Firmicutes; B.
Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Hypothetical protein SAV0719.
SAV0719 OR SA0674.
                                                                                                              Q99VQ4
Q99VQ4;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical 31.6 kDa protein.
ATIG58210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry,
Spermatophyta; Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of the cyclodextrin glucanotransferase gene from alkalophilic Bacillus sp. A2-5a and analysis of the raw starch-binding domain."; Appl. Microbiol. Biotechnol. 53:430-434(2000).

EMBL; AB015670; BAA31529.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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NCBI_TaxID-3702;
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6; Conser
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Pred. No. 52;
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Matches
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Q9C730;
Q9C730;
Q9C730;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation updat Hypothetical 135.5 kDa protein.
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                                                                                 Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. COLUMBIA;

MEDLINS-21016719; Pubmed-11130712;

MEDLINS-21016719; Pubmed-11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Chan H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Feng J.-D., Fong B., Fujli C.Y.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujli C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Minc T. Kremenstryaja T. French V. Kran A., Khaykin E.,
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thaliana.";
Nature 408:816-820(2000)
EMBL; AC073943; AAG50957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AP003360; BAB56881.1; -

EMBL; AP003131; BAB41907.1; -

InterPro; IPR000917; Sulfatase.
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Bacillus/Clostridium group; Bacillales;
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9 SEGULT 19 SEGU
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Q8ZTW7
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
RA Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Etgu P., Feldblyum T.Y., Feng J.-D., Fong B., Fujii C.Y.,
RA Glil J.E., Goldsmith A.D., Haass B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin Hooper S., Lee A., Lee J.M., I-Enz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nterman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 141.0 kDa protein.
T18174.12.
Q8ZTW7;
Q8ZTW7;
Q1-MAR-2002
01-MAR-2002
01-JUN-2002
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Q9C6Q9;
01-JUN-2001
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AC079131; AAG50760.1; -.
InterPro; IPRO01064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 1246 AA; 140995 MW; BE23EE9DC47F3F88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. COLUMBIA;
MEDLINE=21016719; PubMed=11130712;
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                                                                                                          PRELIMINARY;
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85.7%;
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85.7%;
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Pred. No.
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update)

Hypothetical protein PAE3058.

Thermoproteaceae; Pyrobaculum aerophilum.

Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;

Pyrobaculum.

NCBI_TaxID=13773; [1]

STRAIN-IM2 / ATCC PubMed-11792869; SEQUENCE FROM N.A.

51768 / DSM 7523;

Fitz-Gibbon S.T., Ladner H.,

Kim U.-J.,

Stetter K.O.,

Simon M.I.,

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RESULT 15
QBUKI 1
QBUKI 1
AC QBUKI
DT QBUKI
DT Q1-JU
DT Q1-JU
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DT Q1-JU
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Matches 6
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MEDLINE-21608550; PubMed-11743193;

Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McCragelland E., Palmieri A.,

Ruymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.

Gordon-Kamm B., Liao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Mester E.W.,
                                                                                                                                                                                                        Science 294:3317-2233(2001).
EMBL; AE0008936; AAL45803.1; -.
Plasmid: Complete proteome.
SEQUENCE 92 AA; 10349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8UKI9:
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; SEQUENCE 79 AA; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the hyperthermophilic crenarchaeon aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009908; AAL64642.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens (strain C58 / ATCC 33970).
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NCBI_TaxID-176299;
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                                                                                                                                                                                                                                                                                                                                     genome of the natural genetic engineer Agrobacterium tumefaciens
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5; Conserv
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27
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95 MW; B36D5871B6C30143 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha subdivision; Rhizobiaceae
                                                                                                score 30; DB; Pred. No. 25; Pred. No. 25; Mismatches
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Search completed: November 12, 2002, 17:00:20 Job time : $4.13305 \ \text{secs}$

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Minimum DB
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(AMGE-) AMGEN INC

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AAE15495	AA014136	AAE15498	AA014132	AAO14133	AA014135	AAU09900	AAE15493	AAU75408	AA014130	ABB81488	AAU99512	AAY71914	AAE09240	AAY94000	AAB36312	AAW75783	AAU10949	AAE09244	AAE15494	AAW75785	AAE15500	AAU10951	AAY94006	AAE15492	AAE15491	AAE15489	AAE15490	AAY71980	AAB08844	AAB60700	AAE15486	AAE15501	σ	AAE00507
. Human TACI cystein			Protein of hTACI (Protein of hTACI (Protein of N-termi		Human transmembran	Tumour necrosis fa	trans			Human tumour necro	Human TACI protein	A transmembrane ac		Human lymphocyte s	Human AGP-3 recept	Human TACI splice	Human TACI extrace	_	Human TACI cystein	Human AGP-3 recept	A murine ztnf4, a	ਲ	Human-murine B cel	Mouse BCMA-human i		е В се	acid	BAFF re	Human B-cell matur	Все		Human BCMA-Immunog

ALIGNMENTS

RESULT 1
AAE15485
ID AAE15485;
XX
AC AAE15485;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human B-cell maturation (BCMA) protein extracellular domain.
XX

Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TRVF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.

Homo sapiens.

WO200187979-A2.

22-NOV-2001. 2001WO-US15567.

12-NAY-2000; 2000US-204039p.
27-JUN-2000; 2000US-214591.

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RESULT 2
AAE15484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF CC family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI of TACI or BCMA. The method is useful for treating B-cell or T-cell CC lymphoproliferative disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL BCMA and TACI CC antagonists are useful for treating inflammation and immune function CC diseases such as diarrhoed, psoriasis, aligrates, pneumonia, atopic CC dermatitis, respiratory allergic disease (asthma, bypersensitivity lung CC disease), drug and insect sting allergy, inflammatory bowel disease (C (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer CC with leucocyte infiltration of the skin or organs. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                   Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; panorreatic; prostate; Inflammation; immune disorder; diarrhoea; psoriasis; colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                WO200187979-A2.
                                                                         Domain
                                                                                                                                                                                                                                                                        drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human B-cell maturation (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE15484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (BCMA) activity in a mammal. The method comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention activator and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE15484 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family ligand
                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                         rheumatoid arthritis; atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAGOCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCMA protein extracellular domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to a method for inhibiting TACI (transmembrane intracellular CAML interactor) and/or B cell maturation
                                                                     /note= "Cysteine-rich consensus region; This is region is specifically claimed as SEQ ID NO: 7 in claim 1 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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                                                    Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 51;
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                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc activator and intracellular CAML interactor) and/or B cell maturation cc protein (BCWA) activity in a mammal. The method comprises administering ca specific binding partner for APRIL (G70, a tumour necrosis factor-TWRF CC family ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA in a memmal which is useful for inhibiting activity of TACI/CC and/or BCMA in a memmal which is useful for treating B-cell or T-cell CC lymphoproliferative disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI/CC antagonists are useful for treating inflammation and tumoure function CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic CC dermatilis, respiratory allergic disease (asthma, hypersensitivity lung CC disease, colitis) scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus crythematosus), fungal, CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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27-JUN-2000;
14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                           BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
                                                                                                                                                                                                                              02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-2001.
                                               Domain
                                                           Key
                                                                                                                                                                                                                                                               AAB08843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC
                                                                                                Homo
                                                                                                                                                                                              Amino acid sequence of human
                                                                                                                                                                                                                                                                                               AAB08843 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with leucocyte infiltration of the skin or organs. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                              MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCMA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-204039P.
; 2000US-214591P.
; 2001US-0214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 10A; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US15567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     relates to a method for inhibiting TACI
                                             Location/Qualifiers 57..77
                               /note= "putative transmembrane domain"
                                                                                                                                                                                                                                                                                             peptide; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 239; DB 23;
Pred. No. 1.6e-21;
; Mismatches 0;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for
                                                                                                                                                transmembrane activator and CAML-interactor; tumour necrosis factor; znff4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus crythematosus; mysathenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; remain reposes; multiple myeloma; lymphoma; light chain neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a BCMA (not defined) polypeptide. BC is a necrosis factor (NF)-kB activator. The method of the invention used to identify compounds which modulate BCMA activity (and thus NF activity). The specification describes a method of identifying a
                                                                                          immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension;
                                                                                                                                                                                                                                                                        Human; BR43x2; TACI receptor;
                                                                                                                                                                                                                                                                                                            A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                AAY94001 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2000; 2000WO-US04925
WO200040716-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 45
                                                                           artery stenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEN HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 7A; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that modulate NF-kB expression and thus for drug
                                                                             occlusion; cholesterol; renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                      extracellular domain; BCMA; B cell protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 239; DB 21;
Pred. No. 1.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Human; TNF; TNFR; TACI;

WO200160397-A1 Homo sapiens psoriasis. Human BCMA protein 19-NOV-2001

(first

entry)

Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF recept TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymbo autoimmune disease; rheumatoid arthritis; multiple sclerosis;

TNF receptor;

AAE09241 RESULT

AAE09241 standard; Protein; 184

8

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AAE09241;

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                                                                                                                                                                                          CC protein) receptor contain a cysteine rich domain, and are used for chihibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used CC for inhibiting BR43X2, TACI or BCMA receptor-ligand engagement associated CC with activated or resting B lymphocytes, effector T-cells, or with cC antibody production. The antibody production is associated with an . CC autoimmune disease selected from systemic lupus erythematosus, myasthenia CC gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity CC and BR43X2, TACI or BCMA receptor-ligand engagement is associated with CC asthma, bronchitis, emphysema, end stage renal failure, CC glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, CC amyloidosis, moderating immune response, immunosuppression, graft cersus host disease, joint pain, swelling, anaemia, or CC septic shock. BR43X2, TACI, and BCMA polypeptides, fusions, antibodies, CC agonists or antagonists can be used to treat hypertension, renal artery CC stenosis, or occlusion, and cholesterol or renal emboli.
                                                                                Matches
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor TACI is a tumour necrosis factor (TNF) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 152; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1999;
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                                                                                                                                                             Sequence
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                                        1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
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MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                 Similarity
                                                                                                                                                             184
                                                                                Conservative
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                                                                                               100.0%;
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                                                                          Score 239; DB 21;
Pred. No. 1.7e-21;
Pred. No. 1.7e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as loukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                  gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCMA; B cell maturation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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22-AUG-2000;
  06-OCT-1999;
11-FEB-2000;
                                                                               05-OCT-2000; 2000WO-US27579
                                                                                                                                      12-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE00506 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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DB; AAD15902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B cell maturation protein (BCMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Proliferation Inducing Ligand Receptor; APRIL-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; F1g
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  99US-0157933
2000US-0181807
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2000US-0226986
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Pred.
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. NO. 1.7e-21;
smatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic;
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5

WO200112812-A2 Homo sapiens Lymphoma;

gene

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AAB60698

AC AAB6

XX

DT 22-H

XX

Huma

KW Huma

B - CC

KW Orggy

KW Autc

KW Orggy

KW Orggy

KW Orggy

Homo

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Homo

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Homo

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PN WO20

PN WO20

PD 22-F
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                          Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; remour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is human APRIL-R also referred as BCMA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reacing a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma prostate carcinoma, and other carcinomas whose proliferation is modulated APRIL. It is also useful for treating autoimmune diseases (Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                       Human BAFF receptor (BAFF-R)
                                                                                                                                                                                                                                                                                                                                                              22-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD03844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOJ ) BIOGEN INC.
(APOT-) APOTECH R & D SA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100
l Similarity 100
42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; Protein; 184
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Pred. No. 1.7
); Mismatches
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. No. 1.7e-21;
smatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rennert P;
                                                                                                                                                                                                                            hypertension;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AAV7199 ID AAV779 JID AAV779 JID AAV779 AC AAV77 XX AV7 28-b DZ Huma XX Huma KW Tuma KW there KW there
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Best Local :
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11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TWF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R, specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Innibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus crythematosus, autoimmune haemolytic anaemia suppression in the suppression of the systemic lupus crythematosus, autoimmune haemolytic anaemia suppression in the suppression of the systemic lupus crythematosus, autoimmune haemolytic anaemia.
                                                                                             Human: Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autolimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the use of a BAFF receptor (BAFF-R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Fig 1; 59pp; English
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                                                                                                                                                                                                                                                                      Human B cell maturation factor (BCMA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71979 standard; Protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence
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thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16; post-streptococcai glomerulonephritis; polyarteritis nodosa; BCMA;
                                                                                                                                                                                                                                                                                                                                          28-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity nes 42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
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APOTECH R /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0149378.
2000US-0181684.
2000US-0183536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents human BAFF-R.
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Pred. No. 1.7e-21;
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RESULT 9 ABB81487

ABB81487 standard;

Protein;

184

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ABB81487;

02-SEP-2002

(first entry)

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В
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                                                               Matches
                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                         maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
                                                                                                                                                                                                                                                                                         autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Tumour necrosis factor (TNF) and ApoL-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 37; Page 104-105; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocyte proliferation, used autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI:
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01-MAY-2000;
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                                                                                                                                                                         spleen and lymph nodes but not by brain, muscle, heart, pancreas, testis and placenta. BCMA mRNA is absent in t lymphocyte stage but its expression increases with B ly
                                                                                                                                                                                                                       useful in diagnostic assays.

The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated TALL-1 protein is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation
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                              ب
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DB; AAD02125.
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                              MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                               42;
                                                                               Similarity
                                                                                                                               184
                                                               Conservative
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2000US-0201012
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                                                                                                                               AA;
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                                                                            Score 239;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to identify compounds that regulate
                                                               Mismatches
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                                                             DB 22;
..7e-21;
s 0;
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receptor

related protein SEQ

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NO: 7

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The present invention describes a human tumour necrosis factor receptor CC designated Enfr12 (I). (I) has cytostatic, immunosuppressive, designated Enfr12 (I). (I) has cytostatic, immunosuppressive, CC dermatological, antinflammatory, neuroprotective, antidiabetic, and hypotensive CC entirities, and can be used in gene therapy. (I) can be used for CC (e.g. 2004), for treating disorders and disease associated with BCC (e.g. 2004), for treating disorders and disease associated with BCC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for CC (e.g. 2004), for treating disorders and disease associated with BCC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for CC (e.g. 2004), for treating disorders and disease mellitus, and for CC (e.g. 2004), for treating CC (e.g. 2004), for conclusion and disorders such as systemic lupus erythematosus, myssthenia (CC (e.g. 2004), for conclusion and gomerulonephritis, vasculatis, chronic lymphoid CC (e.g. 2004), for conclusion, and polonephritis, and for treating renal failure (CC (e.g. 2004), for explones, lymphomas, light chain neuropathy, or CC (e.g. 2004), for modulating the immune system, for regulating B cell responses and CC (e.g. 2004), for modulating the immune system, for regulating B cell responses and CC (e.g. 2004), for modulating and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention.
                                                                                                                                        Matches
                                                                                                                                                                          Query Match
Best Local
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20-DEC-2000; 2000US-257131P.
28-JUN-2001; 2001US-301715P.
29-AUG-2001; 2001US-315565P.
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                                                                                                                                                                                                                                                                                Sequence
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                                         MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated human tumor necrosis factor receptor polypeptide, termed 12, useful for treating autoimmune disorders, emphysema, end
                                                                                                                                    1 Similarity
42; Conser
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                                                                                                                                                                                                                                                                                184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                failure or renal disease and
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ę
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                                                                                                                                Score 239; I
Pred. No. 1.7
); Mismatches
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No. 1
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                                                                                                                                DB 23;
L.7e-21;
s 0;
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MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV

42 42 Matches

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Indels

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Loca1

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RESULT 10
AAE15488
ID AAE15
                                                                           CC protein (BCMA) activity in a mammal. The method comprises administering CC a specific binding partner for April (G70, a tumour necrosis factor TNF femily ligand), having the consensus region of TACI, BCMA, or the TACI/CC BCMA extracellular consensus sequence, but not the extracellular region CC of TACI or BCMA. The method is useful for inhibiting activity of TACI CC and/or BCMA in a mammal which is useful for treating B-cell or TACI CC appropriate at the disorders, one or more solid tumours such as lung, CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic cdisease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitts), scleroderma, autoimmune disease (multiple cselerosis, rheumatoid arthritis, systemic lupus crythematosus), fungal, CC bacterial, protozal and viral infections (HTV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence cc is human BCMA protein-immunoglobulin Fc region fusion protein.
                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       administering family ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colifis;
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention activator and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 10B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-2000; 2000US-204039P.
27-JUN-2000; 2000US-214591P.
14-MAY-2001; 2001US-0214591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-2001; 2001WO-US15567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; canc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2002
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                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-066686/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; atherosclerosis; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCMA - immunoglobulin
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 1 Similarity
42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane activator and intracellular CAML interactor; TACI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             relates to a method for inhibiting TACI (transmembrane intracellular CAML interactor) and/or B cell maturation
                                                                           AΑ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
Score 239; I
Pred. No. 2.6
); Mismatches
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                 239; DB 23;
No. 2.6e-21;
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RESULT 11
AAEOUSTO
LD AAEOUSTO
AC AAEOUSTO
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11-FEB-2000;
30-JUN-2000;
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The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BGM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulate by APRIL. It is also useful for treating autoimmune diseases (Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE00507 standard;
                                                                                                                                                                                                                                                                                                                                                                    Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering composition comprising A Proliferation Inducing Ligand Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (APOT-)
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                                                                                                                                                                                                                                                                                              1; Fig
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; 2000US-0181807.
; 2000US-0215688.
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                                                                                                                                                                                                                                                                                              3B; 85pp; English.
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24..30
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76..30
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/note- '
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/note= "Derived from mu
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RESULT 12
AABBOLT 12
AABBOLT A
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1999;
11-FEB-2000;
18-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus crythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                                                                                                                              Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polyperide, chimeric molecule comprising receptor or anti-BAFF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                               (BIOJ )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human BAFF-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse
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                                                                                                                                                                                                                                                                                                                                                              Mackay F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-2000;
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DB; AAF59999.
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                                                                                          4; Fig
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                                                                                                                                            homolog
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                                                                                                                                                                                                                                                                                                                                                           Browning
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; 2000US-0183536.
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2.8e-21;
s 0;
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as BCMA) protein, or a treatment of a variety

invention relates to the use of a BAFF receptor (BAFF-R, also known BCMA) protein, or a BAFF-R fusion protein as an agent for the atment of a variety of immune-related disorders. BAFF-R is a member

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production.
          activator and administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; tymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psortasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human B cell maturation protein cysteine rich extracellular region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents the BAFF-R fusion protein BAFF-R-FC, comprising a mouse IgG-kappa signal sequence, residues 1-153 of human BAFF-R and a human IgG Fc sequence.
Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor
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27-JUN-2000;
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Pred. No. 2.8e-21;
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Inhibiting activity of B

cell maturation protein and/or transmembrane

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AAE15486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI or BCMA. The method is useful for treating B-cell or TACI or BCMA in a mammal which is useful for treating activity of TACI clamboprolliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease, (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region.
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Best Local
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27-JUN-2000;
14-MAY-2001;
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                                WPI; 2002-066686/09
                                                                                                                                                                                                                                                                                                                                                                                    Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; canc
                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhea; psoriasis; colliis;
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                                                                                                          (AMGE-) AMGEN INC.
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                                                                  rheill LE,
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                                                                                                                                                                                                                                                                                                                                                                                                                          tate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-cell maturation (BCMA) protein cysteine-rich consensus region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane activator and intracellular CAML interactor; TACI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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; 2000US-214591P.
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Pred. No. 1
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune-related disorder: B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB60700 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535
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MacKay F, Browning J,
                                                         (BIOJ ) BIOGEN INC
(APOT-) APOTECH R
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18-FEB-2000;
                                                                                                                                                                                                                     17-AUG-1999;
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20000S-0183536.
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Tschopp J,
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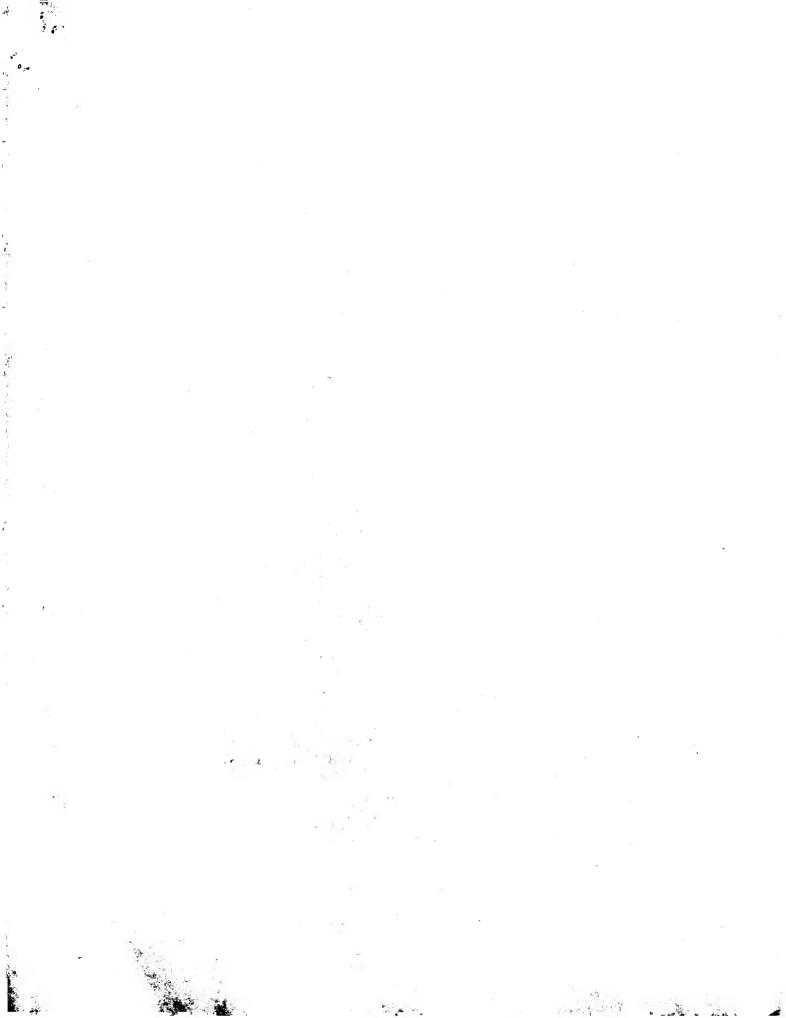
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1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV MAG---QNEYFDSLLHACIPCQLR---NTPPLTCQRYCNASV

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CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the TNF (tumour necrosis factor) family, acting as an immunoregulatory cagent, and also plays a role in the development of hypertension and created disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory cagent, and also plays a role in the development of hypertension and created disorders. BAFF-R, fusion proteins containing it, and BAFF-R cospecific antibodies can be used for inhibiting B-cell growth, dendritic call-induced B-cell growth and maturation, and immunoglobulin production. Cand in the treatment of autoimmune disorders, B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, compressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF-R thereby inhibiting inflammation. Since BAFF-R conhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, cardiagenessive disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive disease, multiple myeloma, B-cell acrcinomas, leukaemia, rapidly chuman BAFF-R may be used in gene therapy to treat tumours, lymphomas, accorders. The accomposers and inharited B-cell-associated disorders. Brechenge as accorded to the composition of the second content accorders and inharited B-cell-associated disorders.
  Matches
                                                   Query Match
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antibody homolog -
                                                                                                                                                          present sequence represents a human BAFF-R protein sequence as encoded
by plasmid PJST535. However, this BAFF-R protein sequence is 27 amino
acids shorter than that given in AAB60698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor
                                                                                                         Sequence
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US-08-815-815-81-4
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US-08-815-895-33
US-08-90-42-105-2
US-09-042-105-2
US-09-042-105-12
US-09-042-105-12
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US-08-795-430-8
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Query Match 28.2%; Score 67.5; DB 2; Length 166; Best Local Similarity 30.6%; Pred. No. 0.61;	US-08-810-572A-6 US-08-810-572A-6 Sequence 6, Application US/08810572A Patent No. 5963102 GENERAL INFORMATION: APPLICANT: Bram, Richard J. APPLICANT: Promition: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: ILLYMPHOCYTE SURFACE RECEPTOR THAT BINDS TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THE SAME AND TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THE SAME AND TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THE SAME AND TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THE SAME AND TITLE OF INVENTION: THEREOF NUMBER: 10 A JOCKSON, ESG. STREET: 411 Hackensack STREET: 411 Hackensack STREET: PlooT STREET: New Jersey COUNTRY: USA ZIP: 07601 COMPUTER: IBM PC COMPATION COMPUTER: THAN PC COMPATION MEDJUM TYPE: Floopy disk COMPUTER: THAN PC COMPATION: DECENTANTE PALCATION NUMBER: US/08/810,572A FILLING DATE: 28 FEB-197 CLASSIFICATION NUMBER: US/08/810,572A FILLING DATE: 28 FEB-1997 CLASSIFICATION INFORMATION: REGISTRATION NUMBER: 35,742 REFERENCE/DOCKET NUMBER: 340-1-007 TELEPHONE: 201-487-5800 TELEPHONE: 201-487-5800 TELEPHONE: 201-487-5800 TELEPHONE: 301-487-5800 TELEPHONE: 301-487-5800 TELEPHONE: 301-487-5800 TELEPHONE: SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 166 amino acids TYPE: amino acids TYPE: amino acids TYPE: MOLECULE TYPE: N-cerminal ORIGINAL SOURCE: N-cerminal ORIGINAL SOURCE: N-cerminal ORIGINAL SOURCE: N-cerminal	ALIGNMENTS	28 53.5 22.4 77 2 US-08-486-399-4 Sequence 29 53.5 22.4 77 2 US-08-486-399-40 Sequence 30 53.5 22.4 77 2 US-08-641-965-4 Sequence 31 53.5 22.4 77 2 US-08-641-965-4 Sequence 32 53.5 22.4 77 2 US-08-634-641-4 Sequence 33 52.4 77 2 US-08-634-641-4 Sequence 34 53.5 22.4 77 2 US-08-634-641-4 Sequence 35 52.4 77 2 US-08-634-641-4 Sequence 36 53.5 22.4 77 3 US-09-249-471-4 Sequence 37 53.5 22.4 77 3 US-09-249-472-4 Sequence 38 53.5 22.4 77 3 US-09-249-451-4 Sequence 40 53.5 22.4 77 3 US-09-249-451-4 Sequence 41 53.5 22.4 77 3 US-09-249-451-4 Sequence 42 53 5 22.4 77 3 US-09-249-451-4 Sequence 43 53.5 22.4 77 3 US-09-249-451-4 Sequence 43 53.5 22.4 77 3 US-09-249-451-4 Sequence 44 53.5 22.4 77 3 US-09-249-451-4 Sequence 45 53.5 22.4 77 3 US-09-249-461-4 Sequence 46 53.5 22.4 77 3 US-09-249-461-4 Sequence 47 53.5 22.4 77 3 US-09-249-461-4 Sequence 48 53.5 22.4 77 3 US-09-249-461-4 Sequence 49 53.5 22.4 77 3 US-09-249-461-4 Sequence 40 53.5 22.4 77 3 US-09-249-461-4 Sequence 41 53.5 22.4 77 3 US-09-249-461-4 Sequence 42 53 5 22.4 77 3 US-09-249-461-4 Sequence 43 53.5 22.4 77 3 US-09-249-461-4 Sequence
6;	AND METHODS OF USE		uence 4, Appli uence 40, Appli uence 40, Appli uence 40, Appli uence 41, Appli uence 42, Appli uence 43, Appli uence 44, Appli uence 44, Appli uence 45, Appli uence 46, Appli uence 47, Appli uence 47, Appli uence 48, Appli uence 48, Appli uence 49, Appli uence 49, Appli uence 41, Appli uence 41, Appli uence 41, Appli uence 42, Appli uence 43, Appli uence 44, Appli

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application Patent No. 6316222 GENERAL INFORMATION:
Sequence 2, Application US/08810572A
Patent No. 5969102
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE
                                                                                                                                                                                                                                                                               Best
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                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                    5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA 40
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
STREET: 411 Hackensack Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                    CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 68
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                                                                                                                                                                                                                                                                           Similarity
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TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Bulow, Gotz
 A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
                                                                                                                                                                                                                                                         28.2%; Score 67.5; DB
30.6%; Pred. No. 0.61;
tive 9; Mismatches
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Continental Plaza,
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US-09-290-333-2
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US-08-810-572A-2
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Best Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810.5
FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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CORRESPONDENCE ADDRESS:
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                          TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                             COUNTRY:
                                                                                                           STATE: New Jersey
                                                                                                                             CITY: Hackensack
                                                                              ZIP: 07601
SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                         Richard J.
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9; Mismatches
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Pred. No. 1
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                                                                                                                                                            Continental Plaza,
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Version #1.30
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ATTORNEY/AGENT INFORMATION:

CLASSIFICATION: <Unknown> FILING DATE: 12-Apr-1999 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

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Patent No. 5851817
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APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
APPLICANT: Garbers, David L.
                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino aci
                                                                                                                              REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of TITLE OF INVENTION: Sperm
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Kitchell, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                           TELEFAX: /1.
TELEFAX: 79-0924
                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: Submit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STRANDEDNESS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 293 amino acids
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                                2476 amino acids
                                                                                                            713-789-2679
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                                                                                                                                                                                                                                                            Submitted Herewith
                                                                                                                                                                                                   Barbara S
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Pred. No. 1.
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                                                                                                                                             RESULT 7
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                                                                                                 Patent No.
                                                                                                           Sequence 4,
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                GENERAL INFORMATION:
                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,388 FILING DATE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1851 CSAHSVYTSCVPSCLPSCQDPEGQCTGAGAPSTCEEGC 1888
APPLICANT: CAO, LIAI TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                           3933 ECPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 3964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MORIKAWA, MINORU
APPLICANT: HARADA, NAOKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: FOLLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity nes 12; Conserv
                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                               , Application US/08999811 5932540
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                                               HU, JIN
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SYSTEM: PC-DOS/MS-DOS
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                                                               JING-SHAN
                                  LIANG
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                                               CRAIG A.
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   VASCULAR ENDOTHELIAL GROWTH FACTOR 15
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Pred. No. 4.7e+02;
6; Mismatches 13;
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Pred. No. 1.9e+02;
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; SEO ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: HOMO sapiens
US-08-824-996-2
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US-08-824-996-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.0 Matches 14; Conservative
                                  Query Match
                                                                                                                                                                                                                                                   APPLICANT: Rosen, Craig A.
APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth
TITLE OF INVENTION: Factor 2
                                                                                                                                               EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/824,996B CURRENT FILING DATE: 1997-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08 FILING DATE: 06-JUN-1995 ATTORNEY/AGENT INFORMATION: NAME: MARKOWICZ, KAREN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local 5.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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Similarity 35.0%;
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35.0%;
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                                Score 54.5;
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                  Pred. No. 41;
Mismatches
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                              Length 350;
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RESULT 10
US-08-510-133A-33
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US-09-042-105-4
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GENERAL INFORMATION:
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                                                                                                                                  Matches
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                           TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (202)371-2600
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APPLICANT: CAO,
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                                                                 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/465,968 FILING DATE: 06-JUN-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                               Local
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                                                                                                 4 OCSONEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
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                                                                                                                                  Conservative
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35.0%;
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                                                                                                                                              Score 54.5;
Pred. No. 41;
                                                                                                                                  Mismatches
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Sequence 33, Application US/08510133A Patent No. 6221839
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari

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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Receptor Ligand
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                        STREET: Chicago
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                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                    FILING DATE:
                                                                                                                                                                                                                                                  COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Joukov, Vladomir TITLE OF INVENTION: Receptor Ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gass, David A. REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
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                                                                                                      US/08/585,895
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Pred. No. 41;
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                            Query Match
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               Best Local Similarity
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                                                                                                              TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                    REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 06-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US FILING DATE: 8-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
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                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                     TOPOLOGY:
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CLASSIFICATION:
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              22.8%;
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Pred. No. 41;
                            Score 54.5;
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Mismatches
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               49;
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RESULT 14
US-09-042-105-18
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US-09-042-105-2
Sequence 18, Application US/09042105
PATENT NO. 6640157
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
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                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202371-2600
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
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APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
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APPLICATION NUMBER: US 0
FILING DATE: 06-JUN-1995
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                                                                                                                                    327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                         Score 54.5;
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RESULT 15
US-08-795-430-8
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                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Alitalo,
APPLICANT: Joukov, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)371-254
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NAME: ERIC K. STEFFE
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                            APPLICAMT: JOUKOV Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 57
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                                                                                                                                                                                                                                                                                              327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACECTES 365
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                                CITY: Chicago
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 COUNTRY:
                                              STREET:
                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                              4 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
            Illinois
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                                            E: Marshall, O'Too
6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202)371-2540
                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                            Vascular Endothelial Growth Factor C (Verotein and Gene, Mutants Thereof, and
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                                              O'Toole,
lower, 233
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Pred. No. 4
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South Wacker Drive
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SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-430-8
Search completed: November 12, 2002, 17:01:42 Job time: 6.76824 secs
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PILING DATE:

PRIOR APPLICATION 435

PRIOR APPLICATION NUMBER: PCT/F196/00427

APPLICATION NUMBER: PCT/F196/00427

FILLING DATE: 01-AUG-1996

PRIOR APPLICATION NUMBER: 08/671,573

FILLING DATE: 28-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,132

FILLING DATE: 14-FEB-1996

PRIOR APPLICATION NUMBER: 08/585,895

FILLING DATE: 12-JAN-1996

PRIOR APPLICATION NUMBER: 08/510,133

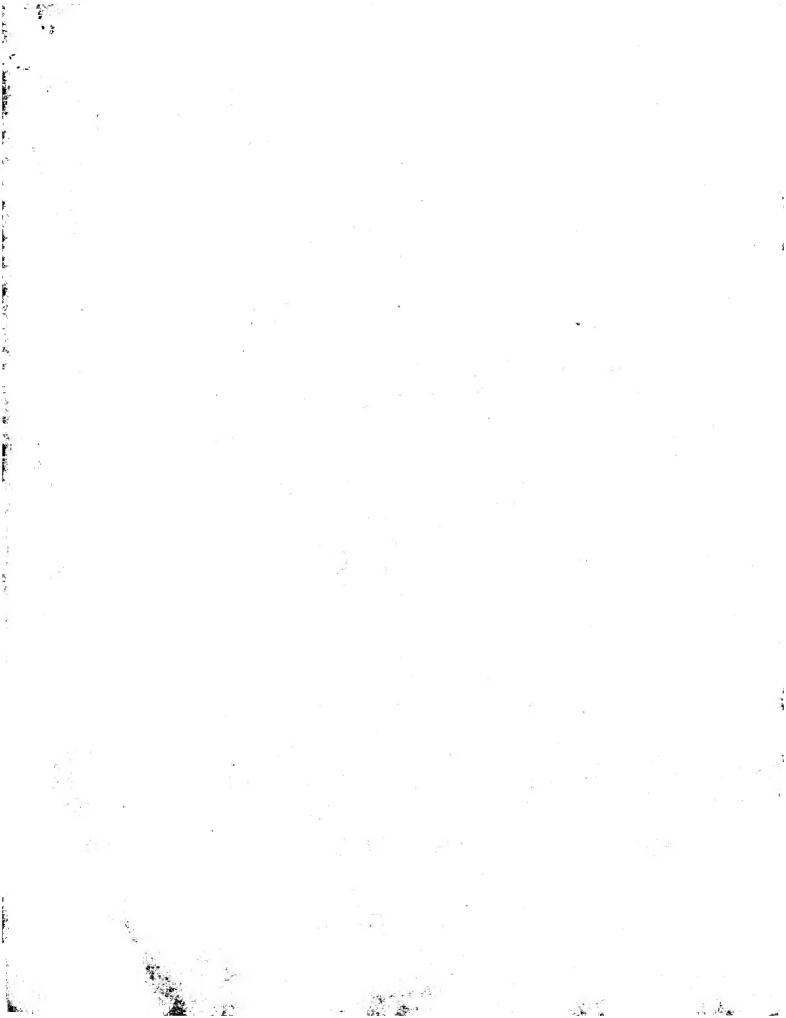
APPLICATION NUMBER: 08/510,133

FILLING DATE: 01-AUG-1995

PRIOR APPLICATION NUMBER: 08/340,011

APPLICATION NUMBER: 38,153

DEFERDENCE COCKETT NUMBER: 28/957/3369;
                                                                                                                                                                                                                                           Query Match 22.8%; Score 54.5; DB 4; Length 419; Best Local Similarity 35.0%; Pred. No. 49; Matches 14; Conservative 2; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
                                                                                                                327 QCGANREFDENTCQCV-CKRTCPRNQPLNPCKCACECTES 365
                                                                                                                                                                         4 QCSQNEYFDSLLHACIPCQLRCSSNTP--PLTCQRYCNAS 41
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
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seq length: 200000000
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12:
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                     l: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2 /cgn2_6/ptodata/1/pubpaa/CCT_NEW_PUB.pep:*
3 /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3 /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
4 /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5 /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6 /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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18 /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 239 239	Match 1	Query Match Length DB 100.0 51 1 100.0 181 1	DB 10	US-09-854-864-6	Description Sequence Sequence
- ω	239	100.0	283	10	US-09-854-864-9	
4 10	219 201	91.6 84.1	3 4 4	10	US-09-854-864-21 US-09-854-864-7	
6	201	84.1	81	10	US-09-854-864-13	
, 7	156	65.3	185	10	US-09-854-864-1	. щ
∞ a	156	65.3	281	10	US-09-854-864-1	35
10	67.5	28.2	37	9	US-09-779-050A-4	U
11	67.5	28.2	59	10	US-09-854-864-2	0
12	67.5	28.2	166	占	US-09-854-864-1	Ċī
13	67.5	28.2	291	9	US-09-779-050A-4	ü
14	67.5	28.2	293	9	US-09-779-050A-4	ົລ
15	67.5	28.2	293	10	us-09-879-919-2	22
16	67.5	28.2	293	10	US-09-854-864-1	4
17	67.5	28.2	293	10	us-09-961-376-2	
18	67.5	28.2	397	10	US-09-854-864-1	œ
19	66.5	27.8	67	10	US-09-854-864-1	φ

ALIGNMENTS

US-09-854-864-6

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; GENERAL INFORMATION:

; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG

; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA

; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
                                                                                                                                                                       RESULT 2
US-09-854-864-5
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                                                                                                                            ; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    y Match 100.0%; Score 239; DB 10; Local Similarity 100.0%; Pred. No. 3.2e-22; hes 42; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-854-864-5
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CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
Sequence 21, Application US/09854864
Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TAGI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 9
LENGTH: 283
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Best Local
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
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ORGANISM: Homo sapiens
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US-09-854-864-13
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US-09-854-864-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09854864 Patent No. US20020081296A1
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SOFTWARE: PatentIn versi
SEQ ID NO 21
LENGTH: 58
                                                                       SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09854864 Patent No. US20020081296A1
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Best Local
ORGANISM: Consensus
:-09-854-864-13
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                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION UNMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI FILE REFERENCE: A-686B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: THEILL, APPLICANT: YU, GA
                                                                             NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentTr
                                                                                                                                                                                                                                                                                               APPLICANT: THEILL, APPLICANT: YU, GA
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TYPE: PRT
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                                     TYPE: PRT
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Pred. No. 8.4e-20;
0; Mismatches 0;
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                                                                                                                               ; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
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Patent No. US20020081296A1
GEMERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
TITLE OF INVENTION: METHODS AND TAGI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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Best Local Similarity
Matches 29; Conserv
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APPLICANT: THEILL, LA
APPLICANT: YU, GANG
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SEQ ID NO 11
LENGTH: 185
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Best Local
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
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                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 31
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1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
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34; Conser
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Pred. No.
                                                                       Score 156; DB 10;
Pred. No. le-11;
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Pred. No. 7e-12;
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                                                                                       Length 281;
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; Sequence 20, Application US/09854864
; Patent No. US20020081296A1
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US-09-854-864-12
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GENERAL INFORMATION:
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Best Local Similarity 30.6%;
Matches 11; Conservative
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APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
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                                                                                                                                                                                                                                                                                                                                  LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                              2 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS 36
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                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                  Score 67.5; DB Pred. No. 0.044;
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Pred. No. 6.4e-05
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APPLICANT:

THEILL, LARS EYDE

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Gaps

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WS-09-779-050A-43
Sequence 43, Application US/09779050A
Patent No. US20020160416A1
GENERAL INFORMATION:
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US-09-854-864-15
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US-09-854-864-15
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US-09-854-864-20
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LENGTH: 59
TYPE: PRT
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Patent No. US20020081296A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                         CURRENT APPLICATION NUMBER: US/09/779,050A CURRENT FILING DATE: 2001-02-12
                                                                                                                     APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
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PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
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PRIOR APPLICATION NUMBER: 60/181,800 PRIOR FILING DATE: 2000-02-11 NUMBER OF SEQ ID NOS: 52
                                                                                                 FILE REFERENCE: A-570B
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: A-686B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: THEILL, LARS EYDE APPLICANT: YU, GANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/204,039 PRIOR FILING DATE: 2000-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1
TYPE: PRT
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Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-779-050A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-879-919-22
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Yu, Guo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application US/09779050A Patent No. US20020160416A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09879919 Patent No. US20020064829A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 43
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                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR PPLICATION NUMBER: 60/277,978
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/276,248
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
FILE REFERENCE: PF253P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
                                                                                                 PRIOR APPLICATION NUMBER: 60/
PRIOR TLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RECEPTOR FROM THE FAMILY
FILE REFERENCE: A-570B
                                                                                                                                                                                                       PRIOR FILING DATE: 2001-03-16 PRIOR APPLICATION NUMBER: 60/254,875
                                                           PRIOR APPLICATION NUMBER: 08 PRIOR FILING DATE: 1997-03-1
                                                                                                                                                                                     PRIOR FILING DATE:
                   PRIOR FILING DATE:
                                          PRIOR APPLICATION NUMBER: 60/016,812
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TYPE; PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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Pred. No. 0.31;
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SEPTIMARE: PatentIn ver. 2.1

SEQ IN NO. 25 LENGTH: 23;

PRESENT 23;

PRESENT 23;

OURLY MAICH 20.48; Score 67.5; DB 10; Length 293;

Best Local Similarity 30.48; Pred. NO. 0.31;

Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

OY 5 CSONEYFDSLLHACIPCOLORGSNTPPLTCORYGN 40

Db 34 CPEDYMDELLOTOMSCNTICHROS-ORTCARFCKS 68

Search completed: November 12, 2002, 17:09:12

Job time: 3.44464 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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622.203 Million cell updates/sec
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SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
52	52	52	52	52	52	52	52.5	52.5	52.5	53	53	53	53	53.5	53.5
21.8	21.8	21.8	21.8	21.8	21.8	21.8	22.0	22.0	22.0	22.2	22.2	22.2	22.2	22.4	22.4
1483	1474	1077	689	547	304	56	847	389	118	596	592	294	274	927	915
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S30015	D88550	T41146	T52060	T34318	JC2264	JN0380	D72860	T29488	S61051	F88188	JC1480	T23682	FB6276	T21772	T21773
hypothetical prote	protein ZC84.6 (im	probable cysteine-	protein MEDEA [imp	hypothetical prote	tissue factor path	trypsin inhibitor	viral capsid assoc	hypothetical prote	hypothetical prote	protein C18H9.7 [1	protein kinase C (hypothetical prote	F14L17.2 protein -	hypothetical prote	hypothetical prote

ALIGNMENTS

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 *text_change 21-Jul-2000
C;Date: 27-Jan-1995 *sequence_revision 27-Jan-1995 *text_change 21-Jul-2000
C;Accession: \$43486; \$31208; \$36661
C;Accession: \$43486; \$31208; \$36661
R;Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994

N; Alternate names: BCM protein; BCMA protein; BEL protein

B-cell maturation factor · human

A;Reference number: \$43486; MUID:94218235; PMID:8165126
A;Accession: \$43486

C.J.; Tsapi

A; Molecule type: DNA A; Status: preliminary

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RESULT 2
$34.83
serine proteinase (EC 3.4.21.-) PC6B - mouse
$c:Species: Mus musculus (house mouse)
$C:Species: Mus musculus (house mouse)
$C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
$C:Accession: $34583
$R:Nakagawa, T.; Murakami, K.; Nakayama, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:BCMA
A;Cross-references: GDB:135977; OMIM:109545
A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-184 <LAA>
A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245
R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, (
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                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z14955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 4-184 <LA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S36661
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A; Residues: 1-184 <LA2>
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Best Local
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Pred. No. 1.1e-20;
); Mismatches 0;
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C;Genetics:
A;Gene: CES
A;Introns:
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T16840
                                                                                                                                                                                                                                                      hypothetical protein T10E10.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 *sequence_revision 20-Sep-1999 *te
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: found exclusively C; Keywords: cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Gao, Z.; Garbers, D.L.
J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, A;Reference number: Z22080; MUID:98123114; PMID:9452463
A;Accession: T42215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: sperm-specific membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T42215
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C;Keywords: hydrolase; serine proteinase
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A; Residues: 1-1548 <NAK>
A; Cross-references: GB:D17583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 327, 165-171, 1993
A; Title: Identification of an
A; Reference number: $34583; M
                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1101 <GEI>
A;Cross-references: EMBL,U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1;
A;Experimental source: strain Bristol N2
                                                                                                                                                                                            submitted to the EMBL Data Library, October 1995 A; Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                             C; Accession: T16840
R; Geisel, C.
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C; Function:
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                                                                                                                                                             A; Reference number: Z18588
A; Accession: T16840
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Best Local (
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   Query
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     Match
                                                 CESP:T10E10.4
                                                                                                                                                                                                                                                                                                                                                                                                      4 QCSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECAAVEYWDEGSHRCQPCHKKCSRCSGPSEDQCYTCPR 1188
                                                                                                                                                                                                                                                                                                                                                                         QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC
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14; Conser
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                                  152/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <GAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: U97068; NID: g3327420; PID: g3327421;
                                191/3; 209/2; 283/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in multiple cell adhesion on the apical region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.1%;
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   27
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Pred. No. 8;
5; Mismatches
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5; Mismatches
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Pred. No. 2
   Score
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No. 8;
   66;
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   DB
                                  303/1;
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                                399/3; 421/1;
Length 1101;
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                                  440/1;
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                                  465/1;
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                                                                                                 CESP:T10E
                                  547/3;
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RESULT T25169

hypothetical C; Species: C:

Caenorhabditis

T23F1

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Caenorhabditis

eLegans

elegans

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A; Residues: 1-1299 <CIE>
A; Cross-references: EMBL: Z68888; NID: 91167859;
A; Cross-references: clone Sfurin 6; ovary
                                                                                                                          C;Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predi
F;27-3034/Product: seven-pass transmembrane
                                                                                                                                                                                                                                                                                                                                                                                   seven-pass transmembrane receptor protein precursor - C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te
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                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-3034 <HAD>
                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, Octob A; Description: The Celsr family of novel
                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
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A; Accession: T43251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, January 1996 A; Description: Cloning and functional characteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Cieplik, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T43251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     furin (EC 3.4.21.75) - fall armyworm N;Alternate names: paired basic amino acid cleaving enzyme; C;Species: Spodoptera frugiperda (fall armyworm)
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                                                                                                                                                                            A; Map position:
                                                                                                                                                                                            A; Gene: Celsrl
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                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                         A; Accession: T14119
                                                                                                                                                                                                                                                                                                     A; Reference number:
                                                                                                                                                                                                                                                                                                                                                     R; Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                     T14119
                                                                                                                                                                                                         Genetics
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les 14; Conserv
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                               4 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQ----
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QCKENYYKPPAQDACLPCDCFPHGSHSRACDMDTGQCACKPGVIGRQCN
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Pred.
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7; Mismatches
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                                                                               Score 59.5;
Pred. No. 7:
                                                                                                                                                                                                                         NID: 93800735; PID: 93800736; PIDN: AAC68836.1
                                                                                                                                                                                                                                                                                                                                       October 1997
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                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                             DB 2;
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                                                                                                                            protein #status
                                                                                             Length 3034;
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 C;Accession: T25169
R;Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19990
A;Accession: T25169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-330 <WILD
A;Residues: 1-330 <WILD
A;Cross-references: EMBL:Z81129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:T23F1.6
A;Experimental source: clone T23F1
C;Genetics:
                                                                                                                           epidermal growth factor receptor homolog precursor fluke (Schi N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Schistosoma mansoni
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C:Accession: A45558; S27836
R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.;
Mol. Blochem. Parasitol. 53, 17-32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene en A;Reference number: A45558; MUID:92365727; PMID:1501637
A;Accession: A45558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C23G10.8 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te: C:Accession: T15577 R:Latreille, P.
A;Status: preliminary
A;Molecule type: mRNA
A;Molecules: 1-1717 <SHO>
A;Cross-references: EMBL:M86396; NID:g160957; PIDN:AAA29866.1; PID:g160958
A;Note: sequence extracted from NCBI backbone (NCBIP:111129)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
""" 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Gene: CESP:C23G10.8
A:Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C:Superfamily: Caenorhabditis elegans hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 16/3
C; Superfamily: gliadin
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A; Residues: 1-758 <LAT>
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A; Accession: T15577
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Pred. No.
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Pred. No. 25;
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13;
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                                                                                                                                                                                                                                                                                                                                   fluke (Schistosoma mansoni)
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                                                                                                                                                                           encoding a homologue of
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RESULT A43434

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RESULT
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S07127
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C;Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homol C;Superfamily: fluke epidermal growth factor receptor homolog 1; protein; phosphoprot C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprot F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>F;1018-1323/Domain: protein kinase homology <KIN>F;1026-1034/Region: protein kinase ATP-binding mottif
                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein M02G9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tcC;Accession: T23681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arch. Biochem. Biophys. 232, 143-161, 1984
A;Title: The isoinhibitors of chymotrypsin/elastase from Ascaris A;Reference number: S07127; MUID:84255715; PMID:6564898
A;Accession: S07127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: S07127
R; Babin, D.R.; Peanasky,
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  В
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                                                                                                                                                    A; Introns: 23/3;
                                                                                                                                                                      A; Map position:
                                                                                                                                                                                         A; Gene: CESP: M02G9.1
                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                              A; Experimental source: clone M02G9
                                                                                                                                                                                                                                                A;Cross-references: EMBL:281573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:M02G9.1
                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1513 <WIL>
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A; Accession: T23681
                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library,
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                                     12 DSLLHAC-IPCQLRC-SSNTPPLTCQRYCNAS 41
                                                                                            Local
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DSCQNVCQNVCQGACVSQNSPPAVCQQTCRQS
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15; Conserv
                                                                                            Similarity
                                                                                                                                                  71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
                                                                          Conservative
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                                                                                          24.3%;
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Pred. No.
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Pred. No. 50;
                                                                                          Score 58; DB
Pred. No. 59;
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                                                                                                             Length 1513;
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hypothetical protein T23K8.9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96675
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chong, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
Chin, C.W.; Ching, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
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T20130
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G96675
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C;Superfamily: subtlisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane professional content of the content of th
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A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein procas;Reference number: A43434; MUID:92381036; PMID:1512259
A:Accession: A43434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
c;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_cha
C;Accession: A43434
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A;Residues: 1-1680 <ROE>
A;Cross-references: GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
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A; Residues: 1-502 <WIL>
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A; Accession: T20130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; McMurray, A.
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A;Cross-references: EMBL;Z73971; PIDN:CAA98251.1; GSPDB:GN00023; ČESP:C50H2.3a
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C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 15-Oct-1999
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A;Accession: G96675
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GAS3_ARATH
ZAN, PIG
EZ_DROME
VEGC_HUMAN
MY9B_RAT
MY9B_HUMAN
MY9B_HUMAN
FS3_CANFA
YJUG_YEAST
ALK1_MOUSE
KPCZ_RABIT
KPCZ_MOBE
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P46687 arabidopsis
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O94906 mus musculu
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Moore M., Littau A., Grossman A., Haugen H., Foley K., Blu
Harrison K., Kindsvogel W., Clegg C.H.;
"TACI and BCMA are receptors for a TNF homologue implicate
autoimmune disease.";
Nature 404:995-999(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shu
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J. Immunol. 165:1322-1330(2000).
SEQUENCE
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                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell maturation protein is a receptor for the tumor necrosis tily member TALL-1.";

Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).

FUNCTION: Receptor for TNFSF13B/BLYS/BAFF and TNFSF13/APRIL.

Promotes B-cell survival and plays a role in the regulation humoral immunity. Activates NF'-Kappa-B and JNK.

SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF subcellular Location: Type III membrane protein. Plasma memb and perinuclear Golgi-like structures.

TISSUE SPECIFICITY: Expressed in mature B-cells, but not in
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$31209; $31209.
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                                                                                                                                                                                                                                                                                                                                                                                          AB052772; BAB60895.1;
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A., Johnston J., Mudr1 S., Enselman R.,
                                                                                                                                                                                                                                                                                      Immune response;
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RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Vikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombberts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Wushbaw-Boris A., Yoshida K., Hasenway Y Kawaii H. Kohteniu S.
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Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
"The characterization of murine BOWA gene defines
of the tumor necrosis factor receptor superfamily
                                                                                -i- SUBCELLULAR LOCATION: Type III membrane protein
-i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here
produced by alternative splicing.
-i- TISSUE SPECIFICITY: Detected in spleen, thymus,
heart, and at lower levels in kidney and lung.
-i- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001), -i- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J; TISSUE-Colon; MEDLINE-21085660; PubMed-11217851; Kawai J., Shinagawa A., Shibata K.,
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                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                      Wynshaw-Boris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/c; TISSUE-Spleen; MEDLINE-99061155; PubMed-9846698;
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                                                                                                                                                                                                           FUNCTION: Receptor for TWFSF13B/BLyS/BAFF and TWFSF13/APRIL. Promotes B-cell survival and plays a role in the regulation humoral immunity. Activates WF-kappa-B and JNK (By similarit SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF
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RC STRAIN-C57BL/GJ; TISSUF-Lung;
RX MEDLINE-21089660; PubMed-11217851;
RX MEDLINE-21089660; PubMed-11217851;
RA ARAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Shibata K., Yosawa H., Kondo S., Yamanaka I.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Altawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Hatsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Barsh G.,
RA Sakai K., Oxido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Oxido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local Similarity
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Dixit V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activator and CAML interactor)
TNFRSF13B OR TACI.
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                      "Identification of a humoral immunity.":
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                                                                                                                                                                                                                                                                                                                                                                humoral immunity
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S.A., Grewal I.S.,
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CYTOPLASMIC (POTENTIAL).
TNFR-CYS.
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Pred. No. 1.7e-12;
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                                                                                                                                                                                                                                                                                                                                                                              for BLyS demonstrates a crucial role
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CRC64;
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RESULT 4
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Meng S.-Y., Boyle W.J., Hsu H.,
"TACI is a TRAP-interacting receptor for TALL-1, a
factor family member involved in B cell regulation.
J. Exp. Med. 192:137-143(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20341628; PubMed-10880535;
Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Bo
Theill L.E., Colombero A., Solovyev I., Lee F., N
Miner K., Hawkins N., Guo J., Stolina M., Yu G.,
Meng S.-Y., Boyle W.J., Hsu H.;
Meng S.-Y., Boyle W.J., Hsu H.;
                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                   MGD;
                                                                                                                                                                                                                                                                                                                              modified and this starement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-gib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "TACI-ligand interactions are required for T collagen-induced arthritis in mice.";
                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of Nature 409:685-690(2001).
                                                                                                                                                                                                      DOMAIN
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                                                        Local
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 6
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                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type III membrane protein (Probable) SIMILARITY: CONTAINS 2 THER-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                           domain of CAMLG with
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
                     CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
                                                                                                                                                                                                                                                                                   MGI:1889411;
CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC
                                                                                                                                                                                                                                                                                              AF257673; AAG00081.1;
AK004668; BAB23457.1;
                                             l Similarity
12; Conser
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                                                                                                                                                                                                                                                  Immune
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                                             Conservative
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                                                                                          A
                                                                                                                                                                                                                                        response;
                                                                                                                                                                                                                                             TNFR_NGFR_1; 1.
TNFR_NGFR_2; 2.
response; Signal-anchor; Transmembrane; Repeat.
                                                                                                                                                                                                                                                                                   Tnfrsf13b
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                                                                                          26947 MW;
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                                           Score 71.5; I
Pred. No. 0.05
8; Mismatches
                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
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TNFR-CYS 2.
                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                (POTENTIAL)
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                                                                                       CB2F2D61C2931D81 CRC64;
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 38
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                                                                 Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                      a collaboration - MBL outstation
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                                           Gaps
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Q04592; Q62040;
01-FEB-1995 (Rel. :
16-OCT-2001 (Rel. :
15-JUN-2002 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4.";
J. Biochem. 113:132-135(1993).
                                                                                                                                                                                                                                                                                                 MEDITARE-96293359; PubMed-8698813;
Constam D.B., Calfon M., Robertson E.J.;
"SPC4, SPC6, and the novel protease SPC7
morphogenetic proteins at distinct sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS
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16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Proprotein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5)
(Convertase PC5) (PC6) (Subtilisin-like proprotein convertase 6)
                                                                                         "Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";
Dev. Genet. 21:75-81(1997).
-I- FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPROTEASE ACTIVITY WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PARHWAY. CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE FOR THE MATURATION OF GASTROINTESTINAL PEPFIDES. MAY BE INVOLVED IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                Bendayan M., Seldah N.G.;
"The isoforms of proprotein convertase subcellular compartments.";
J. Cell Biol. 135:1261-1275(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N. "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: candidate proprotein convertase expressed in endocrine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM PC5A)
TISSUB-Brain, and Intestine;
MEDLINE-93224489; PubMed-8468318;
Nakagawa T., Hosaka M., Torii S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION MEDLINE-97103178; PubMed-8947550;
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STRAIN-ICR: TISSUE-Intestine;
MEDLINE-93327934; PubMed-8335106;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                       morphogenetic
J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nonendocrine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakagawa T., Murakami K., Nakayama 
"Identification of an isoform with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCSK5
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                                                                                                                                                                                                                                                        DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC6, a Kex2-like processing endoprotease. BS Lett. 327:165-171(1993).
IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA T OF GROWTH FACTORS.

CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM T PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG--ZAA BOND CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

SUBCELLULAR LOCATION: PC5A IS SERRETED THROUGH THE RE SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natl. Acad.
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                                                                                                                                                                                                                                                                                     proteins at distin
134:181-191(1996).
                                                                                                                                                                                                                                                       EXPRESSION
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Rodentia;
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during embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  are sorted to different
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
                                                BONDS,
                  REGULATED
                                                               THEIR
   LOCALIZED
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                                                WHERE
                                                                                              ACTIVATION
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                                                                                              CHAIN
                                                                                                                                                             Cleavage
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                                                                                                                              SIGNAL
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J. [3]

of.

A PARANUCLEAR POST-GOLGI NETWORK EARLY ENDOSOMES.
ALTERNATIVE PRODUCTS: AT LEAST 2 AT LEAST 2 ISOFORMS; PC5B/LONG COMPARTMENT IN COMMUNICATION WITH (SHOWN

AND PGSA/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PC5A IS EXPRESSED IN MOST TISSUES BUT IS MOST
ABUNDANT IN THE INTESTINE AND ADRENALS. PC5B IS EXPRESSED IN THE
INTESTINE, ADRENALS AND LUNG BUT NOT IN THE BRAIN.
DEVELOPMENTAL STAGE: WEAKLY EXPRESSED THROUGHOUT THE EMBRYO,
EXCEPT IN THE DEVELOPING NERVOUS SYSTEM, THE RIBS AND THE LIVER,
BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT.
BUT MARKEDLY UPREGULATED AT DISCRETE SITES DURING DEVELOPMENT.
E5, PROMIXENT EXPRESSION OBSERVED IN DIFFERENCIATED DECIDUA. A
E6.5, PROMIXENT EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMMION AND A P

E7.5, INTENSE EXPRESSION IN EXTRAEMBRYONIC ENDODERM, AMNION AND NASCENT MESODERM. AT 8.5, ABUNDANT EXPRESSION IN SOMITES AND YOLK SAC FOLLOWED BY A CONTINATION TO DEFMANYOTOME COMPARTMENT BETWEEN E9.5 AND E11.5, ABUNDANT EXPRESSION IN AER (THICKENED ECTODERMAL CELLS OF LIMB BUDS), AT E12.5, EXPRESSION IN THE LIMBS IS CONFINED TO THE CONDENSING MESENCHYM SURROUNDING THE CARTILAGE. AT THIS STAGE, STRONG EXPRESSION ALSO DETECTED IN VERTEBRAL AND FACIAL CARTILAGE PRIMORDIA AND IN THE MUSCLE OF THE INTESTINAL VILLI. ISOFORM A IS MOST ABUNDANT AT ALL STAGES BUT SIGNIFICANT LEVELS OF ISOFORM B OCCUR AT E12.5.

10 CHAIN. THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE ASSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE ENDOPLASMIC RETICULUM.

11 DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN SORTING PROTEIN PACS-1.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB.

11 SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.

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MGD; MGI:97515; Pcsk5.
InterPro; IPR00251; EGF-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR002184; P_domain.
InterPro; IPR002884; P_domain.
InterPro; IPR00209; Peptidase_S8; 1.
Pfam; PF00082; Peptidase_S8; 1.
Pfam; PF00082; Peptidase_S8; 1. EMBL; D17583; BAA04507.1; -.
EMBL; D12619; BAA02143.1; -.
EMBL; D14932; AAA74636.1; -.
PIR; JX0248; JX0248.
PIR; A48225; A48225. PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; 1.
SMART; SM00181; EGF; 3.
SMART; SM00001; EGF_like; 2.
SMART; SM000261; FU; 22. PROSITE; PS00136; PROSITE; PS00137; PROSITE; PS00138; Hydrolase; 099405; S08.076; 9 117 1769 1790 1790 117 Serine pair 1MPT ; SUBTILASE_ASP; 1.
; SUBTILASE_HIS; 1.
; SUBTILASE_HIS; 1.
; SUBTILASE_SER; 1.
e protease; Clycoprotein; Zymogen; Signal;
of basic residues; Repeat; Alternative sp 1768 1789 1877 1877 452 602 34 116 1877 POTENTIAL.
CYTOPLASMIC
CATALYTIC.
HOMO B. EXTRACELLULAR PROPROTEIN CONVERTASE SUBTILISIN/KEXIN splicing;

<u>6</u>.

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for commercia.

collaboration

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RESULT 5
ZAN_MOUSE
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) ZAN_MOUSE
) ZAN_MOUSE
C 088799; 008647;
T 16-0CT-2001 (Rel. 40, Created)
DT 16-0CT-2001 (Rel. 40, Last sequence update)
DT 16-0CT-2001 (Rel. 40, Last annotation update)
T 3-0nadhesin precursor.
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Best Local
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  Gao Z., Harumi T., Garbers D.L.;

"Chromosome localization of the mouse zonadhesin gene (ZAN)";

Genomics 41:119-122(1997).

-1 FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION SIGNALING.

-1 SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-1 SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-1 SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-1 SUBUNIT: REGION OF THE SPERM HEAD.

-1 TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPPING AND ADDITION OF THE SPERM HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
SEQUENCE
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                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                       membrane
                                                                                                                                                                                                                                        MEDLINE=98123114; PubMed=9452463;
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                 MEDLINE-97271566; PubMed-9126492;
                                                                                                                                               TISSUE-Testis
                                                                                                                                                         SEQUENCE OF 4864-5376 FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                 "Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 36.1
14; Conservative
                                                                                                                                                                                                                              Garbers D.L.;
                                                                                                                                                                                                      diversity in the structure of zonadhesin, protein containing multiple cell adhesion
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                                                                                                                                                                                                     protein
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     IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS
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AC 1.
AC 2.
CLEAVAGE (AUTO-) (BY 9
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N-LINKED
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5; Mismatches
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Pred. No. 0
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ATEESWAEGFCWLVKKNNLCQRKVLQQLCCKTCTFQG
(IN ISOFORM PC5A).
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                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FING (IN ISOFORM | EC850E2DF20EA1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
RELAY SYSTEM (BY SIMILARITY).
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ED (GLCNAG. . ) (POTENTIAL).
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                                                              MANNER TO THE RECOGNITION
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EMBL; U83190; AAG
MGD; MGI:106656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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                                                 DOMAIN
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PROSITE; PS01186; EGF_2;
PROSITE; PS00740; MAM_1;
PROSITE; PS50060; MAM_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESTON TO THE OVIDUCTAL ISTHMUS. DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT OLICOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2). SIMILARITY: CONTAINS 3 MAMA DOMAINS. SIMILARITY: CONTAINS 25 VWFD DOMAINS. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     n; PF00094; vwd; 4.
n; PF00629; MAM; 3.
n; PF01826; TIL; 25.
n; PF02345; TILa; 25.
RT; SM00181; EGF; 2.
RT; SM00274; FOLN; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U97068; AAC26680.1; -. U83190; AAC53125.1; -.
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SM00214; VWC;
SM00216; VWD;
                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
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J IPRO03645; Folv.

J IPRO00368; MAN-domain.

J IPRO02919; TIL_Cysrich.

J IPRO03328; TILa_Cysrich.

J IPRO0137; WRF_C.

J IPRO0101846; WRF_D.
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5338
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215
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80 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
(MUCIN-LIKE DOMAIN).
VWED 1 (PARTIAL).
VWED 2.
VWED 3.
VWED 3.
VWED 5 (PARTIAL).
VWED 5 (PARTIAL).
VWED 6 (PARTIAL).
VWED 7 (PARTIAL).
VWED 7 (PARTIAL).
VWED 10 (PARTIAL).
VWED 10 (PARTIAL).
VWED 11 (PARTIAL).
VWED 12 (PARTIAL).
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VWED 19 (PARTIAL).
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POTENTIAL.
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Best Loc
Matches
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0.14836;
0.14836;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last sequence update)
17-JUN-2002 (Rel. 41, Last sequence update)
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DO
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                                                       MEDLINE-97458245; PubMed-9311921; von Buelow G.-U., Bram R.J.; "NF-AT activation induced by a CA
                                                                                                                         SEQUENCE FROM
TISSUE-B-cell
                                                                                                                                                                                        NCBI_TaxID=9606
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This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                    InterPro: IPR001368; TNFR_c6.
PROSITE; PS00652; TNFR_NGFR_1; 1.se_NEG.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Immune response; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                              AF023614; AAC51790.1; -. BC028072; AAH28072.1; -. HGNC:18153; TNFRSF13B.
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Boone T., Delaney J., Hawkins N., Kelley M., Ramakri Boone T., Delaney J., Hawkins N., Guo J., Stolina S., Qiu W.R., Kornuc M., Xla X.-Z., Guo J., Stolina W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.; and TALL-I and receptors BCMA and TACI: system for r
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278:138-141(1997).
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RA Arakawa T. Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno M., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagquer L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagquer L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Carninol P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninol P., De Bonaldo M.F.,
RA Blake J., Bult C., Fletcher C., Flyita M., Gariboldi M.,
RA Blake J., Bult C., Fletcher C., Flyita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Haynshtarki Y.,
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STRAIN-BALB/C: TISSUE-B cell lymphoma;
MEDLINE-21442025; pubmed-11509692;
Thompson J.S., Bixler S.A., Qian F., V
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cell-
   Harless S.M.,
Hilbert D.M.,
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"Identification of a novel receptor for B lymphocyte stimulator is mutated in a mouse strain with severe B cell deficiency.";
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Mammalia; Eutherla; Rodentia;
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Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFRSF13C OR BAFFR OR BCMD OR BR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor 3) (B-cell maturation defect).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9D8D0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yan M., Brady J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21475520; PubMed=11591325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "BAFF-R, a newly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ambrose C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                             MEDLINE=21614654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (J)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol 11:1547-1552(2001)
                                                                                                                                          ional annotation of 409:685-690(2001).
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   Lentz V.M.,
Hayes C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identified TNF
                                                             PubMed=11747827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chan B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
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   Sah A.P., Hs
Cancro M.P.;
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                                                                                                                                                                      full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee W.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
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                                                                                                                                                                         mouse
                              B.L.,
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g_I.D., Mullen
                                                                                                                                                                         CDNA
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                              Clise-Dwyer K.
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Best Local
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sortliin-related receptor (Sorting protein-related receptor containing LDLR class A repeats) (SorLA) (SorLA-1) (Low-density lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR relative with
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SEQUENCE
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Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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peripheral B
  Morwald S., Yamazaki H., Bujo H., Kusunoki J., F
Morisaki N., Nimpf J., Schneider W.J., Saito Y.;
"A novel mosaic protein containing LDL receptor
                                                     TISSUE=Brain;
MEDLINE=97301565; PubMed=9157966;
MEDLINE=97301565; PubMed=9157966;
                                                                                                                                                                                                                                                                                                                                                                                                                                Q98930;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF373847; AAK91827.1; -. EMBL; AK008142; BAB25490.1; -.
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                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Archosaurıa;
                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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                                                                                                                                                                   NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 OCSONEYFDSLLHACIPCOL 23
                                                                                                                                                                                                                                                               ligand-binding repeats) (LR11) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is not detectable. B-cell lymphopoiesis is normal, but the life span of peripheral B-cells is much reduced. SIMILARITY: CONTAINS 1 THER-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: B-cell receptor specific for TMRSF13B/TALL1/BAFF/BLyS. Promotes the survival of mature B-cells and the B-cell response. SUBCELLULAR LCCATION: Type III membrane protein (Probable). ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2: are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Event European Bioinformatics Institute. There are no restream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detected at lower levels in lung and thymus.

DISEASE: Defects in TNFRSF13C are a cause of severe B-cell deficient strain A/WySnJ has a 4.7 kb i in the BAFFR gene leading to an altered C-terminus. The mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               produced by alternative splicing.
TISSUE SPECIFICITY: Highly expressed
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e splicing.
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11:1986-1989(2001)
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                                                                                                                                                                                                                    Aves; Neognathae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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TNFR-CYS (PARTIAL).
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Pred. No. 0.45;
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OF THE STATE OF THE STATE
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                         , Kusunoki J.,
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                                                   Kanaki T.,
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  elements is highly
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                                                   Seimiya K.,
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TO CONSERVED IN humans and chickens.";

A ARTERIOSCIER: Thromb. Vasc. Biol. 17:996-1002(1997).

A ARTERIOSCIER: THRELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT CONTONING LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT CONTONING LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC AND OF PROTEASES.

COME MAY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEIN OF PRASMA, AND CONTONING THE NECEPTOR OF THAT THE MAJOR CHOLESTEROL CARRYING LIPOPROTEIN OF PRASMA, CONTONING CHOLESTEROL BRINDS THE RECEPTOR-CONTONING THE RECEPTOR AND CHOLESTEROL LEVELS LACK REGULATORY EFFECTS ON THIS RECEPTOR.

CONTONING THE MAJOR CHOICE STATUS AND CHOLESTEROL LEVELS LACK REGULATORY EFFECTS ON THIS RECEPTOR.

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CONTONING THE MAJOR CHOICE THE MAJOR CLASS A DOMAINS.
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SMART; SM00160; EN3; 1.
SMART; SM00192; LDLGa; 11.
SMART; SM00135; LY; 5.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01209; LDLRA_1;
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PROSITE; PS01106; EGF 2: 1.

PROSITE; PS01209; LDLRA_1; 11.

PROSITE; PS50168; LDLRA_2; 11.

Endocytosis; Receptor; EGF-like domain; Repeat; Glycoprotein; LDL;

Lipid transport; Cholesterol metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00041; fn3; 1.
Pfam; PF00057; ldl_recept_a; 11.
Pfam; PF00058; ldl_recept_b; 5.
Pfam; PF02012; BNR; 5.
PFRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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ween the Swiss Institute of Bioinformatics and the EMBL outstation-
European Bioinformatics Institute. There are no restrictions on its
by non-profit institutions as long as its content is in no way
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o; IPR003961; FN_III.
o; IPR002860; GH_BNR.
o; IPR002172; LDL_recept_A.
o; IPR000033; Ldl_receptor_rep.
      EGF-LIKE.

LDL-RECEPTOR CLASS A
LDL-RECEPTOR CLASS 
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                                                                        TISSUE-Ependymocyte;

MEDLINE-96338614; PubMed-8743952;

MEDLINE-96338614; PubMed-8743952;

Gobron S., Monnerie H., Meiniel R.,

Lamalle D., Dastugue B., Meiniel A.;

"SCO-spondin: a new member of the the

"SCO-spondin: a new member of the the
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01-0CT-1996 (Rel. 34, Last seq
16-0CT-2001 (Rel. 40, Last ann
SCO-spondin (Fragment).
                            aggregation.";
J. Cell Sci. 109:1053-1061(1996)
                                                         "SCO-spondin: a new member of the thrombospondin family secreted the subcommissural organ is a candidate in the modulation of neu-
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartiodi Bovidae; Bovinae; Bos.
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P98167;
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 SUBCELLULAR LOCATION: Extracellular
               FUNCTION: INVOLVED IN THE MODULATION
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15; Conservative
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PROSITE; PS01285; FA58C_2; 1
PROSITE; PS01209; LDLRA_1; 3
PROSITE; PS50068; LDLRA_2; 3
PROSITE; PS50068; LDLRA_2; 3
PROSITE; PS50092; TSP1; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00057; ldl_recept_a: 3
Pfam; PF00099; tsp_1; 4.
Pfam; PF000093; vvc; 1.
Pfam; PF000754; F5_F8_type_C; 1
Pfam; PF01875; T1L; 1.
SMART; SM00231; FA58C; 1.
SMART; SM00192; LD1a; 3.
SMART; SM00192; LD1a; 3.
SMART; SM00209; TSP1; 4.
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SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.

SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.

SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.
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SM00214;
 Similarity
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IPR001007; VWF_C
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25.1%;
42.9%;
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EGF-LIKE 1.
EGF-LIKE 2.
TSP TYPE-1 2.
F5/8 TYPE C.
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LDL-RECEPTOR CLASS
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15-JUN-2002
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035161;
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Hadjantonakis A.-K., Sh
Hoovers J.M.N., Little
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mCelsrl is an evolutionarily conserved seven pass transmembrane receptor and is expressed during mouse embryonic development."; Mech. Dev. 78:91-95(1998).
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Mammalia; Eutheria;
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                              + + + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transmembrane receptor, maps chromosome 22qter.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                            mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome
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                                                             TISSUE SPECIFICITY: Expressed in the brain, where it is localized principally in the ependymal cell layer, choroid plexus and the area postrema. Also found in spinal chord and in the eye.

SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                            signaling during nervous system formation.

SUBCELULAR LOCATION: Integral membrane protein.

BUELDPHENIAL STAGE: First detected at E6. Predominantly expressed in the developing CNS, the emerging dorsal root ganglia and cranial ganglia. In the CNS, expression is uniform along the rostrocaudal axis. During gastrulation, it is expressed in the vicinity of the primitive streak, and becomes predominant in that area at late gastrulation. At E10, detected in ventricular zones (VZ), but not in marginal zones (WZ), and weakly in other structures. Between E12 and E15, a high expression is present in
                                                                                                                                                                                                                 the VZ in all brain areas. No expression in differenciated neuronal fields. In the newborn and postnatal stages, expression
                                                                                                                                                                                         kidney and epithelia.
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-C57BL/6; TISSUE-Brain;
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                                                                                                                                                                                                       VZ. Also found
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R Pfam; PF00008; cadherin; 9.

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R PRINTS; PR00011; EGF_AMMIN; 1.

R PRINTS; SM00180; EGF_Lam; 1.

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R PROSITE; PS00650; G_PROTEIN_RECEP_F2_1; FALSE_NE PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.

R PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.

R PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.

R PROSITE; PS00651; G_PROTEIN_RECEP_F2_4; 1.

R PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; PALSE_NE PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; FALSE_NE PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; PALSE_NE PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; FALSE_NE PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; PALSE_NE PROSITE; PS00651; PALSE_NE PRO
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15-JUL-1999 (Rel. 38, Last annotation update)
Chymotrypsin/elastase isolnhibitor 1 (C/E-1 inhibitor).
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
Ascarididae; Ascaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babin D.R., Peanasky K.J., www.The isoinhibitors of chymotrypsin/elastase lumbricoides: the primary structure."; Arch. Biochem. Biophys. 232:143-161(1984).
MEDILINE-92381036; PubMed-1512259;
Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;
"Cloning and functional expression of Dfurin2, a subtilisin-like
proprotein processing enzyme of Drosophila melanogaster with mult
repeats of a cysteine mottf.";
J. Biol. Chem. 267:17208-17215(1992).
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01-APR-1993 (Rel.
15-JUL-1998 (Rel.
                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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-i- SIMILARITY: BELONGS TO THE
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InterPro; IPR000561; EGF-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR002184; P-domain.
InterPro; IPR00209; P-eptidase_S8.
Pfam; PF00002; P-eptidase_S8; 1.
Pfam; PF01403; P-eptidase_S8; 1.
Pfam; PF01403; P-pARFIAL.
PRINTS; PR00723; SUBTILISIN.
PRODOM; PD000717; P-domain; 1.
SMART; SM00181; EGF; 1.
SMART; SM00261; FU; 10. CARBOHYD CARBOHYD DOMAIN CARBOHYD ACT_SITE CHAIN ACT_SITE This SWI between REPEAT REPEAT REPEAT REPEAT PIR; A43434; A43434. HSSP; Q99405; 1MPT. the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an CARBOHYD REPEAT CARBOHYD CARBOHYD CARBOHYD CARBOHYD SIGNAL PROSITE; PROSITE; PS00136; MEROPS; S08.049; -. FlyBase; FBgn0004598; EMBL; M94375; AAA28551.1; -. or send an email to license@isb-sib.ch). entities requires a CARBOHYD CARBOHYD TRANSMEM REPEAT REPEAT REPEAT REPEAT REPEAT DOMAIN PROPEP Multigene нуdrolase; PROSITE; PS00138; European Bioinformatics Institute SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN PS00137; family; 109 130 203 443 481 928 1061 1182 1275 1275 1276 1440 320 418 457 638 962 962 1008 1058 1105 1105 11206 11347 Serine 1533 SUBTILASE_ASP; 1; SUBTILASE_HIS; 1; SUBTILASE_SER; 1 109 130 203 443 481 928 1061 1182 1275 319 418 418 457 638 1444 11007 11057 11104 11205 11205 11346 Zymogen; 1444 1532 1680 protease; license agreement (See http://www.isb-sib.ch/announce/ FURIN-LIKE PROTEASE CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM CHARGE RELAY SYSTEM TO X TANDEM REPEATS, Glycoprotein; N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED N-LINKED POTENTIAL.
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Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                           CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV 42
                                                                                                                                                                                                                                       CGKSAYAVSLLRECV--KLRPSDPTVPLMAAKVCIGSL 312
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595
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                        Conservative
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40,
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Pred. No. 8.7;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                        8B93440B522CFC1C CRC64;
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8.7;
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RA Van der Schueren J. Grymonprez B. Chuang Y.-J. Vandenbussche F. RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Mooljman P., Klein Lankhorst R., Cose M., Hauf J., Koetter P., RA Mooljman P., Klein Lankhorst R., Lanberth S., Van den Daele H., RA Mooljman P., Klein Lankhorst R., Lanberth S., Van den Daele H., RA Dae Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., RA Dan Montagu M., Rogers J., Cronln A., Quail M., Bray-Allen S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ra Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Argiriou A., Vitale D., Liguori R., Piravandi E., RA Mossenet O., Quigley F., Clabauld G., Muendiein A., Felber R., RA Glebdor F., Cocke R., Berger C., Monfort A., Casacuberta E., RA Glebdor F., Cocke R., Berger C., Monfort A., Casacuberta E., RA Glebdor F., Cocke R., Benet E., Johnson S., Tacon D., Jesse T., RA Glebdor F., Kenyel M., Wilson K., Meyes H.-W., Stocker S., RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Parnell P., Bevan M., Wilson R.K., de la Bastide M., Haberman K., RA Parnelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., RA Mensch J., Spieth J., Wanne E., Mordews S., Drone K., Cotton M., Joshu C., RA Antonolu B., Zidanic M., Strong C., Sun H., Lanar B., Yordan C., RA Antonolu B., Zidanic M., Strong C., Sun H., Lanar B., Yordan C., Ra Raby J. K., Marten A., Macomb L., McCombt W., Johnson A., Ra Granat S., Schola M., Marten A., Hamed A.
       between the
the European
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-cv. Columbia;
MEDLINE-20083488; PubMed-10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbi
MEDLINE=95244835;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Welchselgartner M., de Simone V., Obermaler B., Mache R., Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mayer K.F.X., Schueller C.,
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                                                                                                                                                                                                                                       Nature 402:769-777(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vos P.,
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                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                 "Sequence and analysis of chromosome 4 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Langham
                                                                                          TISSUE SPECIFICITY: SILIQUES AND DRY SEEDS PTM: SIX DISULFIDE BONDS MAY BE PRESENT. SIMILARITY: BELONGS TO THE GAST1 FAMILY.
                                                                                                                                                                                       STEPS OF GERMINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .IN=cv. Columbia; TISSUE=Seed; .INE=95244835; PubMed=7727751; .og M., Dorne A.-M., Grellet F.; .i. a gibberellin-regulated gene facted to the tomato GAST1 gene."; .ted to the tomato GAST1 gene."; .ted to the tomato GAST1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T., Duesterhoeft A., Stiekema W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoheisel J., Zimmermann W., Wedler H., Ridley P., S.-A., McCullagh B., Bilham L., Robben J.,
                                                                                                                                                                                                                IN LATE
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                                                                                                                                                                                                                STAGES
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota; Metazoa; (
Mammalia; Eutheria; (
NCBI_TaxID-9823;
[1]
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Q28983;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
or send a
                                                                                        -i- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPEEM HEAD (BY SIMILARITY).
- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS. NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KLDNEY, EPIDIDYMIS.
- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.
- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
- DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUCIN DYMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZONADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX. PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR
                                                                                                                                                                                                                                                                                                    factor.";
J. Biol. Chem. 270:26025-26028(1995).
-I- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U11764; AAB06308.1; --
EMBL; AL161515; CAB78083.1;
EMBL; AL161831; CAB72127.1;
InterPro; IPR003854; GASA,
Pfam; PE02704; GASA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                         <del>: :</del>
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1658-1667; 1777-1795 AND 1914-1921. STRAIN-Meishan; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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             This SWISS-PROT entry
                                                                                                                          +
                                                                                                                                                                                                                                                <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                         *A sperm membrane protein that binds in a cathe egg extracellular matrix is homologous
                                                                                                                                                                                                                                                                                                                                                                                                     Hardy D.M., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96064658; PubMed=7592795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zonadhesin precursor.
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                                      PROCESSING MIGHT OCCUI
CAPACITATION.
- SIMILARITY: CONTAINS:
- SIMILARITY: CONTAINS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (See http://www.isb-sib.ch/announce an email to license@isb-sib.ch).
 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family; Signal.
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a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
is copyright. It is produced through a collaboration stitute of Bioinformatics and the EMBL outstation -
                                      3 4.5 VWFD DOMAINS.
3 1 EGF-LIKE DOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56.5; D
Pred. No. 1.7;
7; Mismatches
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GIBBERELLIN-REGULATED PROTEIN
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\vdash \vdash		Q941u3 oryza sativ	09ep23 hepatitis c	P90891 caenorhabdi	Q8rz84 oryza sativ	Q9vlt6 drosophila	057484 gallus gall	Q9ep28 hepatitis c				Q27422 caenorhabdi	Q9c091 homo sapien	Q9s9j8 arabidopsis		7	O9pvd4 xenopus lae	Ö	Q24301 drosophila		_		Q9vtr9 drosophila	Q26566 schistosoma

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF00094; vwd; 1.
SMART; SM00216; VWD; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gastric mucin-like protein GASTRIC MUCIN-LIKE.
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InterPro; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P56682; 1CCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rio M.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
430 CSQNEYFDHSEGTCVPC-----APPTT
                                                               5 CSONEYFDSLLHACIPCQLRCSSNTPPLT 33
                                                                                                                                                                                                                                                                   499
499 AA;
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                            499
                                                                                                                                                                                                                                                                       54190 MW;
                                                                                                                                                                   30.3%;
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08, Last sequence update)
21, Last annotation update)
ein (Fragment).
                                                                                                                                 1;
                                                                                                                                                                   Score 72.5; DB 11; Length 499; Pred. No. 0.013;
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                                                                                                                                                                                                                                                                           04F89EF4F23EE61E CRC64;
                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00629; MAM; 3.
Pfam; PF01826; TIL; 25.
Pfam; PF02345; TILa; 25.
Pfam; PF00294; vwd; 4.
SMART; SM00001; EGF_like; 1.
SMART; SM00274; FOLK; 21.
SMART; SM00137; MAM; 3.
SMART; SM00214; VWC; 25.
SMART; SM00216; VWD; 4.
  Q9BIO7;
Q9BIO7;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                               PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                    3297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic Basis of Inter- and Intra-species Domain Structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE=21138439; PubMed=11239002; W11son M.D., Rlemer C., Martindale D.W., Schnu Cheung T.L., Hardy D.M., Schwartz S., Scherer Miller W., Koop B.F.; of the gene-dense ACHE/T Chromosome 7922 with the orthologous region on Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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InterPro; IPR003645; Foln.
InterPro; IPR000998; MAM_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                      4 QCSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC
                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; 18.
PS50060; MAM_2; 3.
                                                                                                                                                                                                                                                                                                                                                   domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003328: TILa_Cysrich.
IPR002919: TIL_Cysrich.
IPR001007: VWF_C.
IPR001846: VWF_D.
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  (TrEMBLrel.
                                                                                                                                                                                                                                                Conservative
                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                               Glycoprotein
                                                                                                                                                                                                                                                                 29.18;
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                                                                                                                                                                                                                                           Pred. No. 0.37
5; Mismatches
                                                                                                                                                                                                                                                                                    Score 69.5;
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                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
  sequence update)
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                                                              AA
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                                                                                                                                                                                                                                                                                    DB 11;
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Variation
                                                                                                                                                                3334
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                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region on human
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                                                                                                                                                                                                                                                                                    5374;
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                                                                                      "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank EMBL 193644; AAA80360.2; -. 193644; AAA80360.2; -. 193644; AAA80360.2; -. 19464; AAA80360.2; -. 19464; AAA80360.2; -. 19464; AAA80360.2; -. Chitin_bind_PerA. InterPro; IPR000754; Ketcoacyl-synt. InterPro; IPR003571; Snake_toxin. InterPro; IPR003571; Snake_toxin. InterPro; IPR00359; WRI_EB. 19464; 2. SMARR; SM00289; WRI_EB. 12.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q22378;
Q22378;
PROSITE; PS00606; B_KETOACYL_SYNTHASE; PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN, Hypothetical protein.
SEQUENCE 966 AA; 102460 MW; B565A3C
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HM1:IMSS;
MEDLINE-21428166; PubMed-11545438;
MEDLINE-21428166; PubMed-1154548;
MEDLINE-21428166; PubMed-1154548;
MEDLINE-21428166; PubMed-1154686; PubMed-11546866; PubMed-1154686; PubMed-11546866; PubMed-11546866; PubMed-1154686; PubMed-11546866; PubMed-11546866; PubMed-11546866; PubMed-11546866; PubMed-115468666; PubMed-115468666; PubMed-1154
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00261; FU;
NON_TER 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Profist 152:149-156(2001).
EMBL; AJ409106; CAC34072.1; -.
InterPro; IPR002174; Furin-like.
SMART: SM00261; FU; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-HM1:IMSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geisel C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-5759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                             . elegans
5) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nematoda; Chromadorea;
Cinae; Caenorhabditis.
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Last
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68; DB
Pred. No. 0.09
6; Mismatches
                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cosmid T10E10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFF6362A49F2827A CRC64;
  B565A3CDD25216D9 CRC64;
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annotation update)
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                                                                         UNKNOWN_1
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RESULT
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A Johannson S., Birk R., Hakiy N., Franke P., Kodelja V., Kannicht C.,
RA Orfanos C.E., Johannson S., Goerdt S.;
Orfanos C.E., Johannson S., Goerdt S.;
RT domain-containing adhesion molecules associated with endothelial-
macrophage differentiation and angiogenic processes ";
RI submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ295695; CAC82105-1; -.
DR InterPro; IPR000781; EGF-1ike.
InterPro; IPR000784; Laminin_EGF.
RI InterPro; IPR000561; EGF-1ike.
RI InterPro; IPR000549; Laminin_EGF.
RI InterPro; IPR00058; Link
R Pfam; PF00008; EGF; 20.
R Pfam; PF00008; EGF; 20.
R Pfam; PF00193; Xlink; 1.
DR Pfam; PF00469; Fasciclin; 5.
R Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR PROSITE: SM00415; LINK; 1.
DR PROSITE: SM0045; LINK; 1.
DR PROSITE: PS01186; EGF-1; UNKNOWN_1.
DR PROSITE: PS01186; EGF-2; UNKNOWN_1.
DR PROSITE: PS01186; EGF-2; UNKNOWN_2.
SO SEQUENCE 2551 AA; 276992 MW; 60A44651CCCZBE69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches 13
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Best Local :
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01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                     08R4W8;
08R4W8;
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                                                                                                                  TRAF3 binding protein.
Mus musculus (Mouse).
Eukaryota: Metazoa; Ch
Mammalia; Eutheria; Ro
  SEQUENCE FROM N.A. Mizuno K., Irie S., "Identification of
                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel 01-JUN-2002 (TrEMBLrel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215
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13; Conser
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, Sato T.-A.; novel TRAF3 binding protein, T3BP, which increases
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Primates;
                                                                                                                       Chordata;
Rodentia;
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Last annotation updat
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Last annotation update)
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Pred. No. 0.24
7; Mismatches
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4; Mismatches
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Pred. No.
                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                       Euteleostomi;
; Murinae; Mus
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Friita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Friita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Friita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashtzaki Y., Storch K., Carnincia R., Kandaya M., Jakashtzaki Y., Storch K.-F.,
RA Hayashtzaki Y., Storch K., Kandaya Y., Kawaji H., Kohtsuki S.,
RA Hayashtzaki Y., Storch K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AF350257; AAL83914.1; -.
SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;
                                                                                                                                                                                                                                   Pfam; PF00096; zf-C2H2; 3. ProDom; PD000003; znf_C2H2; 1. SMART; SM00355; znf_C2H2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JUN-2001
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                                                                                                                                                      PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFFC CRC64;
                                                                                                                                                                                                                                                                                             MGD; MGI:1923003; 7420700M05Rik.
InterPro; IPR000822; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL: AK018361: ARB31177.1; -.
HSSP: P08047; 1SP1.
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RCNEREWESQLIRSLPEHGVRCPSQLAPIPFQNYCQRSI 97
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10; Conserv
                                                                                            Similarity
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Last annotation update)
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                                                                                          Score 63;
Pred. No.
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Pred. No.
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1.25;
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RESULT

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026489
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AC 026489
AC 026489
AC 026489
DT 01-NOV-
DT 01-JUN-
DE Endopro
GN FURIN.
OS SPOdopt
OC Pterygo
OC NOCTUOI
ON NCBL_TE
RN [1]
RT fruglip
RL Submit
DR HSSP;
DR Interp
DR Interp
DR Interp
DR Interp
DR Interp
DR Pfam;
DR Pfam;
DR PFAM;
DR PROSIT
  RESERVATION OF THE PROPERTY OF
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01-NOV-1996
01-NOV-1996
01-JUN-2002
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Jenos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG7348
CG7348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1150
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; /
Pterygota; Neoptera;
Ephydroldea; Drosoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00723; SUBTILISIN. ProDom; PD000717; P.domain; 1. SMART; SM00261; FU; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spodoptera frugiperda (Fali armyworm).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VW81;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VW81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00136; SUBTILASE_ASP; PROSITE; PS00137; SUBTILASE_HIS; PROSITE; PS00138; SUBTILASE_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frugiperda (Sf9) cells.";
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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Cleplik M., Klenk H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002174; Furin-like.
InterPro; IPR000209; Peptidase_9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Q99405; 1MPT.
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     Metazoa; Arthropoda; Traches
Neoptera; Endopterygota; Dip
a; Drosophilidae; Drosophila
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(TrEMBLrel. 13,
(TrEMBLrel. 21,
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Last annotation update)
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RA Glodek A. Gong F. Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibegwam C.,

RA Harris N.L., Howland T.J., Wel M.-H., Ibegwam C.,

RA Hostin D., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levttsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levttsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Sylirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;

RT The genome sequence of Drosophila melanogaster.";

DR ENBL; AED03514; AAR49681.] -

DR ENBL; AED03514; AAR49681.] -
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Matches
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   Query Match
Best Local
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01-JUN-2002
01-JUN-2002
                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawge M., Chavez C., Deresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burtis K.C., Busam D.A., Burter ..., Davenport L.B., Davie Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davie de Pablos B., DelCher A., Deng Z., Ways A.D., Dew I., Dd Pablos B., Doub L.E., Downes M., Dugan-Rocha S., Dunton R.
                                                      SEQUENCE
                                                                                         Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                RE16222p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8SZ58;
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                                                                                                            Celniker S.;
                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
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                                                        AY071103; AAL48725.1;
NCE 353 AA; 39712 M
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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(TrEMBLrel.)
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5; Mismatches
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Pred. No. 0
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                     Length 353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8SPM4;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                  Mansouri M., Ey P.L.;
"A segment of a vsp72-like gene homolog from a type A-I Glardia intestinalis isolate.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF298662; AAG37862.1;
EMSP; P00136; 2CY3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glia 32:177-191(2000).
EMBL: AJ416457: CAC94914.1;
SEQUENCE 5146 AA; 543576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovibae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8SPM4
                 InterPro;
InterPro;
                                                 InterPro;
                                                                                                                                                                                                                                Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae;
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCO-spondin.
                                                                                                                                                                                STRAIN-AD-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1814 VFHACVPCPLTCDDISGQATC 1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-SUBCOMMISSURAL ORGAN; MEDLINE-20465125; PubMed+11008217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SUBCOMMISSURAL ORGAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outgrowth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCO-spondin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Subcommissural organ/Reissner's
SCO-spondin, a glycoprotein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meiniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLHACIPCQLRCSSNTPPLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCSVGNYFDPARRACLPVAISAAHQCSCVLPDNATLANPSDCETY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCSQNEYFDSLLHACIPCQL----RCSSNTP------PLTCQRY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conser
 IPR000564; 2Fe2S_ferredoxin.
IPR000345; CytC_heme_bind.
IPR000561; EGF-like.
IPR002174; Furin-like.
IPR002350; kazal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a glycoprotein
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                  Created)
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Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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annotation update)
                                                                                                                                                                                                                                                                                                M21-1 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fiber complex: characterization potent activity on neurite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5146
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9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                  (group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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Best Local S
Matches 15
                                              SMART; SM00112; CA; 9.
SMART; SM00180; EGF_Lam; 1.
SMART; SM00001; EGF_like; 6.
SMART; SM00003; GPS; 1.
SMART; SM00008; HormR; 1.
SMART; SM00082; LamG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
NON_TER
SEQUENCE
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    035161;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57/BL6; TISSUE-BRAIN;
STRAIN-C57/BL6; PubMed-9339365;
MEDLINE-97480720; PubMed-9339365;
Hadiantonakis A.K., Sheward W.J.,
                                                                                                                                                                                                                             Pfam; PF00002; 7tm_2: 1.
Pfam; PF000028; cadherin; 9.
Pfam; PF000028; Egs; 6.
Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 45:97-104(1997).
-!- SIMILARITY: CONTAINS 9
EMBL; AF031572; AAC68836.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                Pfam; PF00053; laminin_EGF; Pfam; PF00054; laminin_G; 1
                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; EGF-like.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; hormn_receptor.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; PKD_cys_rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hadjantonakis A.K., Shew
Hoovers J.M., Little P.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seven-pass transmembrane receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1100883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 22qter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Celsrl, a neural-specific gene
transmembrane receptor, maps to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00749; 1URK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00181; EGF; 2.
SM00001; EGF_like; 1.
SM00261; FU; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.9%;
l similarity 36.6%;
15; Conservative
                                                                                                                                                           FR00205; CADHERIN.
PR00201; EGFLAMININ.
PS00010; ASX_HYDROXYL;
PS00232; CADHERIN_1; 6
PS50268; CADHERIN_2; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00282; KAZAL; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00197; 2FE2S_FERREDOXIN; UNKNOW PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548 AA;
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                                                                                                                                                  GPCRSECRETIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celsrl.
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10,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 CADHERIN DOMAINS
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Last annotation update)
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Pred. No. 1.3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578FE4FDA0A2CF0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse chr
                                 UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harmar A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ing an unusual chromosome 15
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; Murinae; Mus
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RESULT 15
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Best Local S
Matches 15
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Best Local Similarity
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                                                                            O18118
O18118
O18118
O1-JAN 1998 (TrEMBLrel 0
01-JAN 1998 (TrEMBLrel 0
01-DEC-2001 (TrEMBLrel 1
723F1.6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   077419 PRELIMINARY; rn., 077419; 077419; 077419; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Chymotrypsin/elastase inhibitor-1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                     SEOCENCE FROM N.A.
SEOCIENCE FROM N.A.
MEDILINE-98297373; Pubmed-9635450;
Lu C.C., Nguyen T., Morris S., Hill D., Sak
"Anisakis simplex: mutational bursts in the
"Anisakis simplex: mutational bursts in the
SEQUENCE FROM Wilkinson J.;
                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ascaris suum (Pig roundworm)
Eukaryota; Metazoa; Nematoda
Ascarididae; Ascaris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00022; EGF_1; UNKNOWN_6.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01246; LANIUN_TYPE_EGF; UNKNOWN_1.
Calclum-binding; Cell adhesion; EGF-like domain; Glycoprotein; Receptor; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                           Pfam; PF01826; TIL; NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                              serine protease inhibitors from an Exp. Parasitol. 89:257-261(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        EMBL; U94499; AAC61300.1;
HSSP; P07851; LEAI.
                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                               NON TER
                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002919; TIL_Cysrich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-6253;
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                                                                                                                                                                                                                                                     Local Similarity
nes 15; Conser
                                                                                                                                                                                                          4
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                                                                                                                                                                                                        RCGPNEVWTE----CTGCEMKCGDPENTPCPLMCRRPSCECS
                                                                                                                                                                                                                              QCSQNEYFDSLLHACIPCQLRCS--SNTP-PLTCQR-YCNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQ-----RYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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27 30
3034 AA;
                                                                                                                                                                                                                                                                                                   62 AA;
                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                               62
                                             Peloderinae;
            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3034
A; 330477
                                                                                                                                                                                                                                                                                                 62
6794 MW;
                                            Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.98;
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                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                Score 59; DB 5
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Ascaris lumbricoides).
Chromadorea; Ascaridida;
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Pred. No. 6.
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Science 282:2012-2018(1998).
EMBL; Z81129; CAB03405.1; -.
InterPro; IPR003341; DUF139.
Pfam; PP02363; DUF139; 7.
SEQUENCE 330 AA; 36605 MW;
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                                                                                                                                                                                                                  none;
                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-99069613;
                                                                                                                                                                                                      "Genome sequence of the nematode
completed: Nne: 14.7983
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hes 13; Conservative
                                             59 CASSQQYQLQTSQCMPACQQSCSQQCQSNTNTQCQPTCQQSCQTS 103
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                                                                  CSQNEYFDSLLHACIP-----CQLRCSSNTPPL---TCQRYCNAS
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  secs
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